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	ALIGNMENTS US/08700607 Olga Janice ya K. Jennifer L. TWO NOVEL HUMAN NSP-LIKE 9 Pharmaceuticals, Inc. Ette Pharmaceuticals, Inc. Ette BATION: US/08/700,607 UETON: US/08/700,607 UETON: US/08/700,607 US/08/700,607 US/08/700,607 US/08/700,607 US/08/700,115 US/08/700,116	Ω. U
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1318 933 933 1142 11326 11326 11344 1104 11089 11187	ication US/087006 IIIOM: andman, Olga u-Young, Janice coli, Surya K. iillanan, Jannifer WILOW: WINTOW: TWO NOVEL UENCES: IE ADDRESS: IE ADDRESS: I RADDRESS: I RADDRESS: I RADDRESS: ABLE FORM: S. Alto ABLE FORM: S. Diskette Alto Alto CATION DATA: WUMBER: 36,749 COCKET NUMBER: 36,746 COCKET NUMBER: 36,749 COCKET NUMBER: 36,7	nsensus 49. larity 97. Conservative
	Lication 708 Bandman, Bandman, Bandman, Bandman, Bandman, Bandman, Bandman, Bandman, Goli, Sun Hillman, Goli, Sun Go	nsus Lty serv
10000000000000000000000000000000000000	ALIG SULT 1 1.08-700-607-1 2.08-700-607-1 Sequence 1, Application US/08700607 Patent No. 5858708 GENERAL INFORMATION: APPLICANT: Bandman, Olga APPLICANT: Bandman, Olga APPLICANT: Hillman, Janice APPLICANT: Goli, Surya K. APPLICANT: Hillman, Janifer L. TITLE OF INVERTION: TWO NOVEL HUMA NUMBER OF SEQUENCES: 9 CORRESPONDENCE ADDRESS: ADDRESSE: INCYTE Pharmaceutical STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA COUNTRY: U.S. ZIATE: CA COUNTRY: U.S. ZATE: Diskette COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compatible OPERATING SYSTEM: MEDIUM TYPE: Diskette COMPUTER: Flac CAPPATION IN NUMBER: BAPPLICATION NUMBER: BAPPLICATION NUMBER: BF.0114 ATTORNEY/AGENT INFORMATION: TELEPRATION NUMBER: 36,749 REFERENCE/DOCKET NUMBER: 36,749 TELECOMMUNICATION INFORMATION: TELEPRAX: 415-855-0555 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 199 amino acids TYPE: Amino acids TOPOLOGY: linear MOLECULE TYPE: peptide IMMEDIATE SOURCE: LIBRARY:	Consensus -1 Similarity 3; Conserv
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us-09-830-972-2-fused.rai

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APPLICAMT: VENTER, J. Craig et al.

APPLICAMT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOOL307

CURRENT APPLICATION NUMBER: 06/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER: 06/201,498

NUMBER: 0F SEQ ID NOS: 207012

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APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
IITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
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Patent No. 6812339
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Patent No. 5658708
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Au-Young, Janice
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Best Local Similarity 97.3%;
Matches 183; Conservative
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136 PPARPPPPPAGASPLAEPAAPPSTPAAPKRRGSGSSVVDLLYWRDIKKTGVVFGASLFL 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --WERSPAAPAPSLPPA-----AAVLPSKLPEDD----E 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85 VŠSAMDHTFSTTSKDGEGSCYTSLISDICYPPQEDSTYFTGILQKENGHVTISESPEELG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 TPGPSLPDVPGIESRGLFSSDSGIEMTPAESTEVNKILADPLDQMKAEÄYKYIDITRPEE 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            205 VKHQEQHHPELEDKDLDFKNKDTDISIKPEGVREPDKPAPVEGKIIKDHLLEESTFAPYI 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   265 DDLSEEQRRAPQITTPVKITLTRIEPSVETTTQEKTPEKQDICLKPSPDTVPTVTVSEPE 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             325 DDSPGSITPPSSGTEPSAAESQGKGSISEDELITAIKEAKGLSYETAENPRPVGQLADRP 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   504 VRABERAPSRRGLABPGSFLDYPSTEPQPGPELPPGDGALEPETPMLPRK-PEEDSSSNQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 45.3%; Score 826.3; DB 2; Best Local Similarity 27.7%; Pred. No. 7e-29; Matches 195; Conservative 52; Mismatches 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B: Incyte Pharmaceuticals, Inc.
3174 Porter Drive
                                                                                                                                                                                                              MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASISEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0114 US
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF-0114 US
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RESULT 5
US-09-949-016-9180
i Sequence 9180, Application US/09949016
j Batent No. 6812339
j GENERAL INFORMATION:
    APPLICANT: VEWTER, U. Craig et al.
    TILLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
    FILE REFREENCE: LOOU1307
    CURRENT APPLICATION NUMBER: US/09/949,016
    CURRENT FILING DATE: 2000-04-14
    PRIOR FILING DATE: 2000-10-20
    PRIOR FILING DATE: 2000-10-03
    PRIOR FILING DATE: 2000-10-03
    PRIOR FILING DATE: 2000-10-03
    PRIOR FILING DATE: 2000-09-08
    NUMBER OF SEQ ID NOS: 207012
    SOFTWARE: FastSEQ for Windows Version 4.0
    LENGTH: 439
                                                                                               563 SPAATKGPGPLG-----PGAPPPLLFLNKOK----AIDLLYWRDIKQTGIVFGSFLLL 611
                                                                                                                                                                                            LISLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPPRAYLESEVAISEEL 255
                                                                                                                                                                                                                              VQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALIS 315
                                                                 PPARPPPPPPAGASPLAEPAAPPSTPAAPKRRGSGSSVVDLLYWRDIKKTGVVFGASLFL 195
                                                                                                                                                                                                                                                                                                                                                                83 ------APERQPS----- 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            213 LALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIK 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 SFLDYPSTEPQPGPELPPGDGALEPETPMLPRK-PEEDSSSNQSPAATKGPGPLG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44.8%; Score 816.7; DB 4; Length 439;
40.6%; Pred. No. 6.4e-29;
Live 52; Mismatches 101; Indels 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---AAVPPAAAAPLLDFS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               316 LFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 360
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Best Local Similarity 40.6
Matches 182; Conservative
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APPLICAT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1307

CURRENT PAPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

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PRIOR PILING PILING PATE: 2000-10-03
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205 VKHQEQHHPELEDKDLDFKNKDTDISIKPEGVREPDKPAPVEGKIIKDHLLEESTFAPYI 264
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                                                          VQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKPAVLMWVFTYVGALFNGLFLLILALIS :||||::
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                              LLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEEL
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45.3%; Score 826.3; DB 4; Length 776;
Best Local Similarity 27.7%; Pred. No. 7e-29;
Matches 195; Conservative 52; Mismatches 91; Indels 367
                                                                                                                                                                                                                                                                                     316 LFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 360
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Patent No. 6812339
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US-09-949-016-6998
                           196
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                                                                                                  260 SNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSI 319
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                       171 SSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      291 VLAWVFTYVGALFNGLTLILILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQA
  200 TVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37.5%; Score 683; DB 2; Length 208; 67.4%; Pred. No. 1.8e-23;
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bandman, Olga
APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INTENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPENDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                    ||:| :|| || || || || 316 PVVYVKHQAQIDQYLGLVRTHINAVVAKIQAKIPGAKRHAE 356
                                                                                                                                                               320 PVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FASLED Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0114 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/08700607
Patent No. 5858708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                      US-08-700-607-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95 PAAPPAA----PERQPSWERSPAAPAPSLPPA-----AAVLPSKLPEDD----EPPAR 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140 PPPPPPAGASPLAEPAAPPSTPAAPKRRGSGSSVVDLLYWRDIKKTGVVFGASLFILLSL 1999
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                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: AL-YOUNG, Janice
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEB: Incyte Pharmaccuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 EDIDQSSLVS-SSTDSPPRPP--PAFKYQFVTEPEDEE-DEE---
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                                                              333 YLGLANKSVKDAMAKIQAKIPGLKRKAD 360
                                                                                     MEDION TITE: DIBRECTE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 96,749
REGISTRATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 356 amino acids
                                                                                                                                                                                                  Sequence 6, Application US/08700607
Patent No. 5858708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 356 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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CITX: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
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Best Local Similarity 44.1
Matches 177; Conservative
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MOLECULE TYPE:
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US-08-700-607-6
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232 IOKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                             3 SVHDLIFWRDVKKTGFVFGTTLIMLLSLAAFSVISVVSYLILALLSVTISFRIYKSVIQA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                292 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 351
                                                                                                                                                                                                                                                                                                                                                                                                                           172 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA
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                                                                                                                                                                                                                                                                                                                                                                  Length 192;
                                                                                                                                                                                                                                                                                                                                                                                               35; Indela
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; Pred. No. 5.9e-21;
40; Mismatches 35
                                                                                                                                                                                                                                                                                                                                                                 34.3%;
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Best Local Similarity 60.0
Matches 114; Conservative
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183 LPGIAKKKAE 192
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US-09-949-016-8859
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LENGTH: 588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  231 AIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFA 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   291 VLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQA 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 SQAIDLLYWRDIKQTGIVFGSFLLLFSLTQFSVVSVVAYLALAALSATISFRIYKSVLQ 69
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                                                                                                         APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; DB 2; Length 267;
1.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32; Mismatches
                                                                                                                                                                                                                                                                                                                                                       COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: US/08/700,607
ATTONEY, AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
TELECOMUNICATION INFORMATION:
TELECHONE: 415-855-0555
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                                                                                                                Sequence 8, Application US/08700607
Patent No. 5858708
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 267 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
           351 KIPGLKRKAD 360
                                       199 KIPGAKRHAE 208
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Best Local Similarity
Matches 124; Conserv
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LIBRARY: GenBar
CLONE: 281046
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Indels 237;

Length 588;

32.1%; Score 585.3; DB 4; 27.5%; Pred. No. 3.4e-18; ive 52; Mismatches 117;

Query Match 32.1 Best Local Similarity 27.5 Matches 154; Conservative

RESULT

us-09-830-972-2-fused.rai

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CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
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R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,597
R PILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,502
R FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/040,334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/040,626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 563, Application US/09149476 Patent No. 6420526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 1997-03-07
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                                                          241 amino acids
                                                                                                                                                                                                                                Query Match
Best Local Similarity 44.4
Matches 111; Conservative
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                             single
                                                                                                           TOPOLOGY: linear MOLECULE TYPE: peptide IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSKTPWNRQK 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       349 QAKIPGLKRK 358
                                                                                                                                                             LIBRARY: THPINOB01
CLONE: 31870
                                                                         TYPE: amino acid
STRANDEDNESS: si:
                                                          LENGTH:
                                                                                                                                                                                                 US-08-700-607-3
                                                                                                                                                                                                                                                                                                                                                                           169
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                                                                                                                                                                                                                                                  212 EDEEPQEPNKLETGEAGEELDLRLRLAQPS---SPEVLTPQLSPGSGTPQAGTPSPSRSR 268
                                                                                                                                                                                                                                                                                                                                                                                  329 VYKTVPILELSPPLWTAIGWVQRGPTPPTFVLRVLLKWAKSPRSSGVPSLSLGADMGSKV 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                    389 ADLLYWKDTRISGVVFTGLMVSLLCLLHFSIVSVAAHLALLLLCGTISLRVYRKVLQAVH 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----TEGGNDDSDFRELHTAREFSERDEETTSODWGTPREL 105
                                                                                                             106 TFSYIAFDGVVGSGGRRDSTARRPRPQGRSVSEPRDQHPQPSLGDSLESIPSLSQSPEPG 165
                                                                                                                                                                                 ---DPDTAPPSERPLEDLRLRLDHLGWVARGTGSGEDSSTSSSTPL 211
                                                                                                                                                                                                                                                                                                                        269 DSNSGPEEPLLEEEEKQWGPLEREPVRGQCLDSTDQLEFTVEPRLLGTAMEWLKTSLLLA 328
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                                                                                                                                                                                                                                                                                                                                                                                                                              174 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQ 233
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APPLICANT: Au-Young, Janice
APPLICANT: Au-Young, Janice
APPLICANT: Goll, Surya K.
APPLICANT: Goll, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incvr. N.
     SLVSSSTDSPPRPPAFKYQFVTE-PEDEED--
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRAETSD VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0114 US
TELECOMMUNICATION INFORMATION:
                                                                                                                                              65 LSAAAVPPAAAAPLLDFSSDSVPPAPR
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Patent No. 5858708
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COMPUTER READABLE FORM
                                        59 STASSTPDS
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109 ERSPAAPASLPPAAAVLPSKLPEDDEPPARPPPPPAGASPLAEPAAPPSTPAAPKRRG 168
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                                                                                                                                                                                                                                     44 SSCAVHDLIXWRDVKKTGFVFGTTLIMLELARAFSVISVVSYLILALLSVTISFRIYKSV 103
                                                                                                                                                                                                                                                                                                             IQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLK 288
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                                                                                                                                                     ---GAEPSAPGGGGSPGACPA----LGTKSCS
                                                                                                                                                                                                          SGSSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV
                                                     Gaps
                                                  39;
     Length 241;
                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 548.1; DB 2;
; Pred. No. 3e-17;
40; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EARLIER FILING DATE: 1998-03-06
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
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NUMBER: 60/047,633	Ω	5-23	NUMBER: 60/047,617	T.	5-23	NUMBER: 60/047,503	0	: 1997-05-23 MTMDED: 60/047 691	5-23	0	5-23	NUMBER: 60/04/,500 : 1997-05-23	0	5-23	NUMBER: 60/047,492	NIMBER 60/047 598	5-23	0	1997-05-23	5-23		5-23	NUMBER: 60/047,612	1997-09-23 UMBER: 60/047,632	5-23	NUMBER: 60/047,601	40	4-11	NUMBER: 60/043,568	1997-04-11 NITMBER: 60/043 334	4-11	0	1997-04-11 NIMBER: 60/043 311	4-11	φ,	: 1997-04-11 NIMBER: 60/043.674	4-11	NUMBER: 60/043,669	9	4-11	NUMBER: 60/043,313	. 9	4-11	NUMBER: 60/043,315	. 9	90-9	NUMBER: 60/056,886 1987-08-22	9	8-22	NUMBER: 60/056,889 1997-08-32	9	8-22	NUMBER: 60/056,630 1997-08-22	NUMBER: 60/056,878
ATION	EARLIER APPLICATION NUMBER:		APPLICATION	EARLIER FILING DATE: 1997-0 EARLIER APPLICATION NUMBER:		EARLIER APPLICATION DARE.	APPLICATION	EARLIER FILING DATE:	FILING DATE	APPLICATION	EARLIER FILING DATE:	FILING DATE	APPLICATION	FILING DATE:	EARLIER APPLICATION N	APPLICATION	FILING DATE	APPLICATION	EARLIER FILING DATE:	FILING DATE:	APPLICATION	FILING DATE:	EARLIER APPLICATION N	APPLICATION	FILING DATE	EARLIER APPLICATION N	APPLICATION	FILING DATE:	EARLIER APPLICATION N	APPI.ICATION	FILING DATE:	APPLICATION	EARLIER FILING DATE: FARLIER APPLICATION N	FILING DATE:	APPLICATION	EARLIER FILLING DATE: FARLIER APPLICATION N	FILING DATE:	EARLIER APPLICATION N	APPLICATION	FILING DATE:	EARLIER APPLICATION N	APPLICATION	FILING DATE:	EARLIER APPLICATION N	APPLICATION	FILING DATE:	EARLIER APPLICATION N	APPLICATION	FILING DATE:	EARLIER APPLICATION N	APPLICATION	ER FILING DATE:	••	SR APPLICATION

BARLIER FILING DATE: 1997-08-28
BARLIER FILING DATE: 1997-08-28
BARLIER FILING DATE: 1997-08-28
BARLIER FILING DATE: 1997-08-22
BARLIER PAPLICATION NUMBER: 60/056,913
BARLIER PAPLICATION NUMBER: 60/056,913
BARLIER PAPLICATION NUMBER: 60/056,913
BARLIER FILING DATE: 1997-08-22
BARLIER PAPLICATION NUMBER: 60/056,913
BARLIER FILING DATE: 1997-08-22
BARLIER PAPLICATION NUMBER: 60/056,910
BARLIER PAPLICATION NUMBER: 60/057,761
BARLIER PAPLICATION NUMBER: 60/047,586
BARLIER PAPLICATION NUMBER: 60/047,586
BARLIER PAPLICATION NUMBER: 60/047,586
BARLIER PAPLICATION NUMBER: 60/047,586
BARLIER PAPLICATION NUMBER: 60/047,587
BARLIER P

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CORRENT FILING DATE: 1998-09-08

EARLIER APPLICATION NUMBER: PCT/US98/04493

EARLIER FILING DATE: 1998-03-06

EARLIER FILING DATE: 1997-03-06

EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/040,626

EARLIER APPLICATION NUMBER: 60/040,634

EARLIER APPLICATION NUMBER: 60/040,334

EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/040,334

EARLIER FILING DATE: 1997-03-07

EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/040,336

EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/040,336

EARLIER APPLICATION NUMBER: 60/040,336

EARLIER APPLICATION NUMBER: 60/040,336
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CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
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APPLICATION UNDBER: 60/047,615
ALLING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,597
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APPLICATION NUMBER: 60/047,600
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85.7%;
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; ORGANISM: Homo sapiens
US-09-513-999C-6304
                                                           346 AKIQAKIP 353
                                                                                                                                                   196 DKİRVAİP 203
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APPLICANT: Rosen et al.
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Best Local Similarity
Matches 60; Conserv
                                                                                                                                                                                                                                                                                                                                                   US-09-513-999C-6304
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Batent No. 6703491

GENERAL INFORMATION

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Pacentin Ver. 2.0

SEQ ID NO 45132

LENGTH: 219
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29.6%; Score 539.9; DB 4; Length 168;
Best Local Similarity 59.3%; Pred. No. 3.6e-17;
Matches 99; Conservative 36; Mismatches 31; Indels 1
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R APPLICATION NUMBER: 60/056,909
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,875
R APPLICATION NUMBER: 60/056,862
R FILING DATE: 1997-08-22
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,887
RR APPLICATION NUMBER: 60/056,908
R FILING DATE: 1997-08-22
RR APPLICATION NUMBER: 60/056,908
R FILING DATE: 1997-08-22
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R RAPLICATION NUMBER: 60/057,669
R R FILING DATE: 1997-09-05
R R PLING DATE: 1997-06-13
R RPLING DATE: 1997-06-13
R RAPPLICATION NUMBER: 60/061,060
R FILING DATE: 1997-06-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/057,650
FILING DATE: 1997-09-05
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FILING DATE: 1997-06-06
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US-09-270-767-45132
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1 MEDIDOSSLVSSSTDSPPRPPAFKYQFVTEPEDEEDEEBEEBEEDEEDDEDLEELEVLERK
Sequence 6304, Application US/09513999C
Patent No. 6783961
Batent No. 6783961
BAPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Junas Milne Edwards, J.Y.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.US2.REG
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Pred. No. 1.9e-06;
4; Mismatches 4; Indels
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June 23, 2005, 09:56:59; Search time 108.849 Seconds (without alignments) 1271.831 Million cell updates/sec
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1823
1 MEDIDQSSLVSSSTDSPPRP......VKDAMAKIQAKIPGLKRKAD 360
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Maximum Match 100%
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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No.	Score	_	Juery Match Length DB	DB	ID	Description
-	1817	7.66	360	. 6	US-09-893-348-20	Sequence 20, Appl
7	1817	7.66	360	16	US-10-810-653-20	Sequence 20, Appl
e	1808.1	99.2	379	14	14 US-10-205-194-164	Sequence 164, App
4	1732.7		1163	0	US-09-893-348-18	Sequence 18, Appl
S	1732.7		1163	16	US-10-810-653-18	Sequence 18, Appl
9	1637		1162	16	US-10-633-423-10	Sequence 10, Appl
7	1637		1162	16	US-10-427-741-10	Sequence 10. Appl
80	1622.9		1163	15	US-10-267-502-431	Sequence 431, App
Q	1603.3	87.9	373	6	US-09-789-386-6	Sequence 6. Appli
10	1603.3		373	6	US-09-765-205-6	Sequence 6, Appli
11	1603.3		373	6	US-09-893-348-24	Sequence 24, Appl

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4 US-1 5 US-1 6 US-1 7 US-1 6 US-1	9 US-09-789-368-2 9 US-09-893-348-23 9 US-09-893-348-23 1 US-09-893-348-23 14 US-10-060-036-71 15 US-10-267-502-429	16 US-10-466-258-9 16 US-10-466-258-9 16 US-10-810-653-23 15 US-10-408-967-7 9 US-09-893-348-21 16 US-10-810-653-21 9 US-09-893-348-25	US-10-660-946-1 US-10-810-653-2 US-10-408-967-9 US-09-978-360A- US-10-466-258-1 US-10-660-946-28-1 US-10-660-946-28-1 US-10-660-946-28-1	10-723- 10-267- 10-205- 10-660- 10-660- 10-276- 10-106-
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TITLE OF INVENTION ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR US
FILE REFERENCE: EIS-SCHWARTZ-B.
CURRENT FILING DATE: 1039-05-19
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Indels

1 MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTFPRDEEDEEBEBEBEBDEDLEELEVLERK	181 DIKKTGVVFGASLFLILSLTVFSIVSVTAVIALALLSVTISFRIVKGVIQAIQKSDEGHP 24
DD	DD
VDLLYWR VDLLYWR	301
Qy 181 DIKKTGVVFGASLFLLISLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHP 240	RESULT 3 US-10-205-194-164
Qy 241 FRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMWVFTYVG 300	; Sequence 164, Application US/10205194 ; Publication No. US20030134301A1 ; GENERAL INFORMATION: ; APPLICANT: Warner-Lambert Company
Qy 301 ALFNGLTLIILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 360 	; APPLICANT: Lee, Kevin ; APPLICANT: Dixon, Alistair ; APPLICANT: Brooksbank, Robert ; APPLICANT: Pinnock, Robert ; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
RESULT 2 US-10-810-653-20	05,194
Sequence 20, Application US/10810653 Publication No. US20040253218A1 SERRAL INFORMATION:	FRIOR APPLICATION NUMBER: GB 0118354.0 ; PRIOR FILING DATE: 2001-07-27 ; NUMBER OF SEQ ID NOS: 177
AFFLICANT: EASEMAND. STANARIZ, MICHAI APPLICANT: COHEN, Irun R. APPLICANT: OFFEN, Irun R. APPLICANT: APPLICANT: PECTE	SOCIMARS: FARENCIN VET. 2.1 SEQ ID NO 164 "LENGTH: 379
APPLICANT: MOSLEM, ALDINATED TOTAL SILATION OF INVENTIONS AND THEIR USE	
FILE REFERENCE: BIS-SCHWARTZ=ZA CURRENT APPLICATION NUMBER: US/10/810,653 TTRDENT FILING DATE: 2004.03-29	; OTHER INFORMATION: Foocen-m2 reticuion US-10-205-194-164
PRIOR APPLICATION NUMBER: US/09/893,348 PRIOR FILING DATE: 2001-06-28 PRIOR APPLICATION NUMBER: US 09/314,161	Query Match 99.2%; Score 1808.1; DB 14; Length 379; Best Local Similarity 94.7%; Pred. No. 2e-54; Matches 359; Conservative 1; Mismatches 0; Indels 19; Gaps 1;
PRIOR FILING DATE: 1999-05-19 PRIOR APPLICATION NUMBER: US 09/218,277 PRIOR FILING DATE: 1998-12-22 PDDIOR ADDITIONATION NUMBER: DFT/1708/14715	Oy 1 MEDIDOSSLVSSSTDSPPRPPAFKYQFVTEPEDEEDEEEEDDEBLEELEVLERK 60
PRIOR FILING DATE: 1998-07-21 PRIOR APPLICATION NUMBER: IL 124500 PRIOR FILING DATE: 1998-05-19	61 PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPASLP 12
NUMBER OF SEQ ID NOS: 29 SOFTWARE: Patentin version 3.1 SEO ID NO 20	Db 61 PAAGLSAAAVPPAAAAPLIDFSSDSVPPARRGPLPAAPPAAPERQPSWEKSFAAPAFSLP 120 Ov 121 PAAAVIPSKIPEDDEPPARPPPPPAGASPIAEPAAPPSTPAAPKRRGSG 170
LENGTH: 360 TYPE: PRT	
/ ORGANISM: Mattus norvegicus US-10-810-653-20	OY 171SSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 221
Query Match 99.7%; Score 1817; DB 16; Length 360;	Db 181 AASEPVIPSSAVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 240
Matches 359; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
1 MEDIDOSSLVSSSTDSPPRPPAFKYQFVTEPEDEEDEEDEEDEEDEELEVLERK	241
1 MEDIDQSSLVSSSTDSPPRPPRFKYQFVTEPEDEEDEEEDEEDEEDEELEVLERK 60	282 DIVDSLKKAVLMWVFTYVGALFNGTFLLIALISEKSIPVITEKHQVQIDHITGGLANKSV [
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Qy 121 PAAAVLPSKLPEDDEPPARPPPPAGASPLAEPAAPPSTPAAPKRGSGSSVVDLLYWR 180 nh 121 PAAAVLPSKLPEDDEPPARPPPAGASPLAEPAAPPSTPAAPKRGSGSVVDLLYWR 180	Db 361 KDAMAKIQAKIPGLKRKAD 379
141 FRANVLEONDEFFAREFFFFFARANSTANDFARFFFFFFARANGOOGSVVVULLING	RESULT 4 .

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US-09-801-348-18	
; Sequence 18, Application US/09893348	77.
; Patent No. US20020072493A1 ; GENERAL INFORMATION:	Db 601 LPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESF 660
; APPLICANT: BISENBACH-SCHWARTZ, Michal	Qy 172 171
	Db 661 NAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESE 720
: MOALEM, GILA INVENTION: ACTIVATED T-CELLS. NEBUOIS SYSTEM-SPECIFIC ANTICENS	Ογ 172 171
NACO CICLER-SECTION MAILORNO MAD INDIA	Db 721 PVDLFSDDSIPEVPQTQEEAVMLMKESLTEVSETVAQHKEERLSASPQELGKPYLESFQP 780
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; PRIOR FILING DATE: 1999-05-19 ; PRIOR ADDITION NUMBER: 18 04/218 277	Db 781 NLHSTKDAASNDIPTLTKKEKISLQMEEFNTAIYSNDDLLSSKEDKIKESETFSDSSPIB 840
	Qy 172 171
AFFILCATION NOMBER: FC1/US90/14/1 FILING DATE: 1998-07-21 DDTICATION NUMBER: II 194600	Db 841 IIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK 900
; NIMBER OF SEC IN NOS. 29	Ογ 172 171
SOFTIAN STATE OF THE STATE OF THE SEC ID NO. 18	Db 901 DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKED 960
LENGTH: 1 TYPE: PRT ORGANISM:	Qy 172SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS 217
-18	Qy 218 VTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL 277
	Db 1021 VISFRIXKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL 1080
1 MEDIDOSSLVSSTDSPRRPPAFKYQFVTEPEDEEDEEBEBEBEDDEDLEELEVLERK 1	Qy 278 FLVDDLVDSLKFAVLMWVFTYVGALFNGITLLILALISLFSIPVIYBRHQVQIDHYLGLA 337
61	CY 338 NKSVKDAMAKIQAKIPGLKRKAD 360
61 PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP	Db 1141 NKSVKDAWAKIQAKIPGLKRKAD 1163
121 PAAAVLPSKLPEDDEPPARPPPPRAGASPLAEPAAPPSTPAAPKRGSGS	RESULT 5 US-10-810-653-18
DD 121 FAAAVLESKLEEDDEFFARFFFRAGASFLAKFFSTFAAFKKRGSGSVDETLFALF 180 Qy 172 171	; Sequence 18, Application US/10810653 ; Publication No. US20040253218A1 ; GENERAL INFORMATION:
181 AASEPVIPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYL	; APPLICANT: EISENBACH-SCHWARTZ, Michal ; APPLICANT: COHEN, Irun R.
Qy 172 171	; APPLICANT: BESERMAN, Pierre ; APPLICANT: MOSONEGO, Alon ; ADDITONED GILL
241 GNLSAVSSSEGTIEETLANEASKELPERATAPPVARDLAEFSELEYSEMGSSFKGSPKGES	; FILE OF INTENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR US ; FILE REPERENCE: EIS-SCHWARTZ=2A
172	; CURRENT APPLICATION NUMBER: US/10/810,653 ; CURRENT FILING DATE: 2004-03-29
DD 301 AILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDIFNEMQMSVVA 360	APPLICATION NUMBER: US/ FILING DATE: 2001-06-28
361 PVREEYADFKPFEQAWEVKDTYEGSRDVLAARANVESKVDRKCLEDSLEOKSLGKDSEGR	; FRIOR AFFILLION NOTION: 05 09/314,101 ; PRIOR FILING DATE: 1999-05-19 ; PRIOR APPLICATION NUMBER: US 09/218.277
	FILING DATE: 1998-12-22 APPLICATION NUMBER: PCT
Db 421 NEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTSENKTDEKKIEERKA 480	
Qy 172 171	ING DATE: 1998-05-1 SEQ ID NOS: 29
Db 481 QIITEKTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESEL 540	SOFTWARE: Patentin version 3.1 SOFTWARE: Patentin version 3.1 SOFT NO 18 TOWNWARE: 116.2
Qy 172 171	구 없 ;
Db 541 NEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSL 600	; Orcanion: Ratus noivegicus US-10-810-653-18

us-09-830-972-2-fused.rapb

	RESULT 6 US-10-633-423-10 ; Sequence 10, Application US/10633423 ; Publication No. US20040191240A1	; GENERAL INFORMATION: ; APPLICANT: Tohyama, Masaya ; APPLICANT: Yamashita, Toshihide marra on tamamana, Toshihide	NOT NEW YORK	; PKIOR AFFLICATION NUMBER: US 10/42/,/41 ; PRIOR FILING DATE: 2003-94-30 ; PRIOR APPLICATION NUMBER: JP 2003-92923 ; PRIOR PILING DATE: 2003-03-28	; NUMBER OF SEQ ID NOS: 27 ; SOFTWARE: Patentin version 3.1 ; SEQ ID NO 10 ; LENGTH: 1162	s musculus	89.8%; Score 1637; DB 16; Length 1162; ilarity 29.8%; Pred. No. 1.1e-47;	Matches 348; Conservative 2; Mismacches 5; Indels 810; Caps 4; Qy 1 MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEEEEDEEEEDEEEEDEELEVLERK 60	1 MEDIDQSSLVSSSADSPPRPPAPKYQFVTEPEDEEDEE-EEEDDEDLEELEVLERK	Oy 61 PAGGGAAAVPPAAAAPLIDESSISVPPARRGPLAAPPAAPERQPSWEKSFAAPAFSLF 120	121 PAAAVLPSKLPEDDEPPARPPPPAGASPLAEPAAPPSTPAAPKRGSGS 17	Db 119 PAAAVIPSKIPEDDBPPARPPAPAGASPIAEPAAPKRRGSGSVDETLFALP 176	177 AASEPVIPSSAEKIMDLKEQPGNTVSSGQEDFPSVLFETAASLPSLSPLSTVSFKEHGYL	- 17	Db 237 GNLSAVASTEGTIEETLNEASRELPERATNPFVNRESAEFSVLEYSEMGSSFNGSPKGES 296	297 AMLVENTKEEVIVRSKDKEDLVCSAALHNPQESPATLTKVVKEDGVMSPEKTMDIFNEMK	Qy 172 171	357 MSVVAPVREEYADFKPFEQAWEVKDTYEGSRDVLAARANMESKVDKKCFEDSLEQKGHGK	Db 417 DSESRNENASFPRTPELVKDGSRAYITCDSFSSATESTAANIFPVLEDHTSENKTDEKKI 476	Ογ 172 171
Query Match 95.0%; Score 1732.7; DB 16; Length 1163; Best Local Similarity 31.0%; Pred. No. 5.7e-51; Indels 803; Gaps 1; Matches 360; Conservative 0; Mismatches 0; Indels 803; Gaps 1; Qy	Qy 121 PAAAVLPSKLPEDDEPPARPPPAGASPLAEPAAPPSTPAAPKRRGSGS 171 Db 121 PAAAVLPSKLPEDDEPPARPPPPPAGASPLAEPAAPPSTPAAPKRRGSGSVDETLFALP 180	Qy 172	Qy 172	Qy 172 171 Db 301 AILVENTKEEVIVRSKDKEDLVCSAALHSPOESPVCKEDRVVSPEKTMDIFNEMOMSVVA 360	172	172	Db 421 NEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTSENKTDEKKIEERKA 480 Qy 172	481 QIITEKTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESEL	QY 172 171 Db 541 NEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSL 600	Qy 172 171	DD 601 LPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESF 660	661 NAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESE	172	DD 721 PVDLFSDDS1PEVFQTQEEAVMLMAKESLIEVSETVAQHKEEKLSASFQELGKFYLESFQF 780 OV 172	Db 781 NLHSTKDAASNDIPTLTKKEKISLOMEEFNTAIYSNDDLLSSKEDKIKESFTFSDSSPIE 840	172	Db 841 IIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK 900	901 DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKED	172SUVDLLYMRDIKKTGVVFGASLFLLASLTVFSIVSVTAYIALALLS	Db 961 RSLSAVLSABLSKTSVVDLLYWRDÍKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALS 1020 Qy 218 VTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL 277

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	Db 119 PÄÄÄVLPSKÜPEDDEPPÄRPPAPAGÄSPLÄEPÄÄPPÄÄPKÄRGSGSVDETLFALP 176 Qy 172		QY 172	357 MSVVAPVREEYADFKPFEQAWEVKDTYEGSRDVLAARANMESKVDKKCFEDSLEQKGHGK 172	417 DSESRNENASFPRTPELVKDGSRAYITCDSFSSATESTAANIFPVLEDHTSENKTDEKKI	Db 477 EERKAQIITEKTSFKTSNPFLVALHDSEADYVTTDNLSKVTEAVVATMPEGLTPDLVQEA 536 Qy 172	172	Db 597 PLNSLLPSTGASVAQPSASPLEVPSPVSYDGIKLEPENPPPYEEAMSVALKTSDSKEEIK 656 Qy 172 171 Db 657 EPESFNAAAQEAEAPYISIACDLIKETKLSTEPSPEFSNYSEIAKFEKSVPDHCELVDDS 716	Qy 117
Db 477 EERKAQIITEKTSPKTSNPFLVAIHDSEADYVTTDNLSKVTEAVVATMPEGLTPDLVQEA 536 Qy 172	171 716	1/2	· · · · · · · · · · · · · · · · · · ·	YPKDEAHVSDEPSKSRSSVSKVPLLLPNVSALESQIEMGNIVKPKVLTKEAEEKLPSDTE 956	Qy 172SVVDELYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALA 214 Db 957 KEDRSLTAVLSAELNKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALA 1016	QY 215 LLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKEL 274 D DD 1017 LLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKEL 1076 Q	QY 275 RRLFLVDDLVDSLKFAVLAMVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYL 334	Qy 335 GLANKSVKDAMAKIQAKIPGLKRKAD 360 Db 1137 GLANKSVKDAMAKIQAKIPGLKRKAE 1162	RESULT 7 US-10-427-741-10 i Sequence 10, Application US/10427741 i Sequence 10, Application US/10427741 i Sequence 10, Application No. US20040191291A1 i GENERAL INFORMATION: GENERAL INFORMATION: CORRECT: TOHYMARE, TOSHINIGE TITLE OF INVENTION: COMPOSITION AND METHOD FOR NERVE REGENERATION TITLE OF INVENTION: COMPOSITION AND METHOD FOR NERVE REGENERATION CURRENT FILING DATE: 2003-04-30 PRIOR PAPLICATION NUMBER: US/10/427,741 CURRENT FILING DATE: 2003-03-28 NUMBER OF SEQ ID NOS: 25 SOFTWARE: Patentin version 3.1 SEQ ID NO 10 LENGTH: 1162 TYPE: PRT ORGANISM: Mus musculus US-10-427-741-10 Query Match B9: 84; Score 1637; DB 16; Length 1162; Query Match Best Local Similarity 29.84; Pred No 1.1e-47; Matches 348; Conservative 2; Mismatches 6; Indels 810; Gaps 4; ON 1 MEDIDQSSLVSSSTDSPPRPPAFKYQFVTEPEDEEDEEEEEDEEEUERRE 60

7	7/1	657 EPESFNAAAQEAEAPYISIACDLIKETKLSTEPSPGFSNYSBIAKFEKSVPDHCELVDDS	Qy 172 171	Db 717 SPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVSETVTQHKHKERLSASPQEVGKPY 776	Qy 172 171.	Db 777 LESFQPNLHITKDAASNEIPTLTKKETISLQMEEFNTAIYSNDDLLSSKEDKMKESETFS 836	gy 172 171	Db 837 DSSPIEIIDEFPTFVSAKDDSPKEYTDLEVSNKSEIANVQSGANSLPCSELPCDLSFKNT 896	Ογ 172 171	Db 897 YPKDEAHVSDEFSKSRSSVSKVPLLLPNVSALESQIEMGNIVKPKVLTKEAEEKLPSDTE 956	QY 172SVVDLLYWRDIKKTGVV-FGASLFLLLSLTVFSIVSVTAYIAL 213	OY 214 ALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVALSEELVOKYSNSALGHVNSTIKE 273		TOTAL TRADELY PRODUCTION OF THE CONTRACT TO TH	OY 334 LGLAMKSVKDAMAKLQAKLKKAD 360 	RESULT 9 US-09-789-386-6	A1	; APPLICANT: MICHALOVICH, DAVID ; APPLICANT: PRINUHA, NABINDER KUMAR	; IIILE OF INVENIION: NOVEL COMPOUNDS ; FILE REFERENCE GP-30165-C1 ; CURRENT APPLICATION NUMBER: US/09/789,386	; CURRENT FILING DATE: 2001-02-21 ; PRIOR APPLICATION NUMBER: U.K. 9916898.1	; PRIOR FILING DATE: 1999-07-19 ; PRIOR APPLICATION NUMBER: U. K. 9816024.5 ; PRIOR FILING DATE: 1998-07-22	; PRIOR APPLICATION NUMBER: US 09/359,208 ; PRIOR FILING DATE: 1999-07-22	; NUMBER OF SEQ ID NOS: 6 ; SOFTWARE: FastSEQ for Windows Version 3.0	; SEQ ID NO 6 ; LENGTH: 373 manual non	; IYPE: FKI ; ORGANISM: HOMO SAPIENS ; ORGANISM: 4	-03-703-50-0 -03-703-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-	; indels	OY 1 MEDIDOSSLVSSSTDSPRRPPARKYOFVTEPEDEEBEBEBEBEBEBEBLEVLERK 60	:	Oy 61 PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAP 115
1077 RRLFLVDDLVDSLKPAVLMWVFTYVGALFNGLTLLILALISLPSIPVIYERHQAQIDHYL 1136	335 GLANKSVKDAMAKIQAKIPCLKRKAD 360			RESULT 8	. 🖰	Publication No. US20040071700A1 GENERAL INFORMATION:	PPLICANT: Kim, Jaeseob PPLICANT: Galant, Ron	TITLE OF INVENTION: Obesity Linked Genes FILE REFERENCE: LSD-07416	CURRENT APPLICATION NUMBER: US/10/267,502 CURRENT FILING DATE: 2003-01-27	NUMBER OF SEQ ID NOS: 439 SOFTWARE: Patentin version 3.2	3	89.0%; Score 1622.9; DB 15; Length 1163; arity 29.7%; Pred. No. 3.5e-47;	Vacive 2; Mismatches VSSSTDSPPRPPAFKYQFVTEPEDEED	1 MEDIDQSSLVSSSADSPPRPPPAFKYQFVTEPEDEEDEE-EBEDDEDLEELEVLERK 59	61 PAAGLSAAAVPPAAAAPLLDFSSDSVPFAPRGFLPAAPPAAPERQPSWERSPAAPAFSLP 120 	121 PAMAVLPSKLPEDDEPPARPPPPPAGASPLAEPAAPPSTPAAPKRRGSGS 171	FORMALE ONLE BUILDE FOR THE FOREST THE FAIL FOREST FANT FOR THE FANT FOREST TH	177 AASEPVIPSSAEKIMDLKEQPGNTVSSGQEDFPSVLFETAASLPSLSPLSTVSFKEHGYL 236	172	GNLSAVASTEGTIEETLNEASRELPERATNPFVNRESAEFSVLEYSEMGSSFNGSPKGES	172 171 297 AMLVENTKEEVIVRSKDKEDLVCSAALHNPOESPATLIKVVKEDGVMSPEKTMDIFNEMK 356		357 MSVVAPVREEYADFKPFEQAWEVKDTYEGSRDVLAARANMESKVDKKCFEDSLEQKSHGK 416	172 171	417 DSESRNENASFPSTPELVKDGSRAYITCDSFTSATESTAANIFPVLEDHTSENKTDEKKI 476	172 171	EERKAQIITEKTSPKTSNPFLVAIHDSEADYVTTDNLSKVTEAVVATMPEGLTPDLVQEA		CESELNEATGTKIAYETKVDLVQTSEAIQESIYPTAQLCPSFEEAEATPSPVLPDIVMEA	172 171

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Sequence 24, Application US/09893348
; Batent No. US20020072493A1
; Fatent No. US20020072493A1
; GENERAL INFORMATION:
    APPLICANT: BISERBACH-SCHWARTZ, Michal
    APPLICANT: BISERBACH-SCHWARTZ, Michal
    APPLICANT: BESERBACH, Pierre
    APPLICANT: MOSONEGO, Alon
    PRIOR REPERBACE: BIS-SCHWARTZ=2A
    CURRENT APPLICATION NUMBER: US 09/314,161
    PRIOR PILING DATE: 1999-10-22
    PRIOR FILING DATE: 1998-12-22
    PRIOR FILING DATE: 1998-07-21
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       359 AKIQAKIPGLKRKAE 373
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                                                                       RESULT 11
US-09-893-348-24
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US-10-060-036-72
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                                                                                                                                    RG-SGSSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIY
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TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES FILE REPRENEUR: 1458-004/200130.449
CURRENT APPLICATION NUMBER: US/09/765,205
CURRENT FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
LENGTH: 373
TYPE: PRT
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                                               APSLPPAAAVLPSKLPEDDEPPARPPPPAGASPLAE-
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Patent No. US20020034800A1
GENERAL INFORMATION:
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US-09-765-205-6
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US-09-765-205-6
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Length 373;

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APPLICANT: BISENBACH-SCHWARTZ, Michal
APPLICANT: BISENBACH-SCHWARTZ, Michal
APPLICANT: BISERRACH-SCHWARTZ, Michal
APPLICANT: BESERAWA, Irun R.
APPLICANT: BESERRAW, Pierre
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
APPLICANT: MOALEM, Gila
TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR US:
TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR US:
CURRENT APPLICATION NUMBER: US/10/810,653
CURRENT APPLICATION NUMBER: US 09/314,161
PRIOR FILING DATE: 1999-05-19
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: US 09/314,161
PRIOR APPLICATION NUMBER: US 09/314,161
PRIOR APPLICATION NUMBER: US 09/314,161
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PRIOR APPLICATION NUMBER: US 09/314,161
PRIOR PRILING DATE: 1998-07-21
PRIOR APPLICATION NUMBER: US 09/314,161
PRIOR PRILING DATE: 1998-05-19
NUMBER OF SEQ ID NOS: 29
NUMBER OF SEQ ID NOS: 29
NUMBER OF SEQ ID NOS: 29
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                                                          1 MEDLIDOSPLVSSS-DSPPRPQPAFKYQFVREPEDEE-EEEEEEEEEEDEDELEELEVLERK
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87.2%; Pred. No. 2.2e-47;
ative 11; Mismatches 20; Indels
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Best Local Similarity 87.2<sup>3</sup>
Matches 327; Conservative
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US-10-810-653-24
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Publication No. US20040063161A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Pharmacia & Upjohn Company
APPLICANT: Par, Rigiang
APPLICANT: Lu, Yifeng
TITLE OF INVENTION: Compositions and Methods of Treating Alzheimer's Disease
FILE REFERENCE: 00925
CURRENT APPLICATION NUMBER: US/10/408,967
CURRENT FILING DATE: 2003-04-08
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
LENGTH: 373
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                                                                                                                                                                                                                                                                                                                                                                                                                         DB 14; Length 373;
APPLICANT: Lodes, Michael J.
APPLICANT: Persing, David H.
APPLICANT: Heppler, William T.
APPLICANT: Heppler, William T.
APPLICANT: Heppler, William T.
APPLICANT: Jiang, Yuqiu
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REPERENCE: 210121.566
CURRENT APPLICATION NUMBER: US/10/060,036
CURRENT APPLICATION NUMBER: US/10/060,036
CURRENT FILING DATE: 2002-01-30
NUMBER OF SEQ ID NOS: 4560
SOFTWARE: FastSEQ for Windows Version 4.0
EBNGTH: 373
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ORGANISM: Homo sapiens
US-10-060-036-72
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US-10-408-967-8
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US-10-408-967-8
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Search completed: June 23, 2005, 10:34:28 Job time : 113.849 secs

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87.2%; Pred. No. 2.2e-47;
tive 11; Mismatches 20; Indels 17;
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Best Local Similarity 87.24
Matches 327; Conservative
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US-10-347-669-6
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Scoring table:

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Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS; central nervous system; neoplastic disease; antiptoliferative; glioma; antisense gene therapy; neuroblastoma; menagioma; retinoblastoma; degenerative nerve disease; Alzheimer's disease; Parkinson's disease; hyperpoliferative disorder; benign dysprocliferative disorder; benign dysprocliferative disorder; benign dysprocliferative disorder; diagnosis; psociasis; tissue hypertrophy; neuronal regeneration; treatment; structural plasticity; screening; mutant; mutent.
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/note= "Corresponds to residues 975-1162 of
protein shown in AAY71310"
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AAY71311
AAE03987
AAU3328
AAM33484
ADL31138
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AQ16420
ABU11573
AAY95012
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ADO08103
ADP45551
ADP67234
ADR13966
                      ABG30938
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                                                                                                                                                                                                                                                                                              AAY71558 standard; protein; 359 AA
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WO200031235-A2
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Nogo

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This course, and the creatment of neophastic disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, craniophastrogen, cpendyoma, pinealoma, paemangioblastoma, acoustic neuroma, coligodendroglioma, menagioma, medulloblastoma and degenerative perve diseases e.g. Alzheimer's and Parkinson's diseases.

Cligodendroglioma, menagioma, neuroblastoma or retinoblastoma and degenerative or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where neurons or to promote structural plasticity of the CNS in disorders where neurons or to promote structural plasticity of the CNS in disorders where neurons or to promote structural plasticity of the CNS in disorders where neurons or to promote structural plasticity of the CNS in disorders where animal models can be used in diagnostic and screening methods for predisposition to disorders and to screen for or test molecules which can tract or prevent disorders or diseases of the CNS. The present sequence is derived by fusing two fragments of rat Nogo A protein shown in AAY1310. The fragment is used in the construction of mutant Nogo-B. The mutant is composed of His-tagy/rector/Nogo-A sequence an 1-171 + 575-162. Nogo protein. Major inhibitory region was identified in the Nogo attes of Nogo protein. Major inhibitory region was identified in the Asequence from amino acids 172-974, particularly amino acids 542-722. In addition, N-terminal region 1-171 was found to be inhibitory to NHH 373 fibroblast spreading. Note: The present sequence is not given in the SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO; 29 in include sequences for these SEQ ID numbers
   patent relates to neurite growth inhibitor Nogo which is free of all
                                     central nervous system (CNS) myelin material with which it is natively associated. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of
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Sequence 359 AA;

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Rat; neurite growth inhibitor; Nogo B; neural cell; myelin; CNS; central nervous system; neoplastic disease; antiproliferative; glioma;
                                                                                                                           Rat neurite growth inhibitor Nogo B.
                             AAY71383 standard; protein; 360 AA
                                                                                              02-NOV-2000 (first entry)
            AAY71383
ID AAY
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degenerative nerve disease; Alzheimer's disease; Parkinson's disease; ypperproliferative disorder; benign dysproliferative disorder; diagnosis; psoriasis; tissue hypertrophy; neuronal regeneration; treatment; structural plasticity; screening. The present sequence is a rat Nogo B protein which is a potent neural cell growth inhibitor and is free of all central nervous system (CNS) melin material with which it is natively associated. The Nogo B transcript arises as a result of alternative splicing of Nogo gene. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, allohastoma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma, menagioma, neuroblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Nogo proteins and nucleic acids useful for treating neoplastic disorders of the central nervous system and inducing regeneration of neurons. /note= "Corresponds to C-terminal 188 amino acids (residues 976-1163) of Nogo A protein (AAY71310). This region is common to Nogo A, B and C isoforms" 185. .220
/label= Transmembrane domain /note= "C-terminal hydrophobic region" menagioma; retinoblastoma; amino acids 1-172 of Nogo note= "Inhibits NIH 3T3 fibroblast spreading" 287. .322 /label= Transmembrane domain /note= "C-terminal hydrophobic region" 338. .340 'note= "Protein kinase C (PKC) site" site" 'note= "Protein kinase C (PKC) note= "Casein kinase II site" 'note= "Protein kinase C (PKC) /note= "Protein kinase C (PKC) 268. .270 /note= "Asn is N-glycosylated" 'note= "Asn is N-glycosylated" protein shown in AAY71310" "Corresponds to "Acidic region" Location/Qualifiers Example; Page; 122pp; English. 98US-0107446P. 173. .360 31. .58 /note= "? 1. .172 /note= " WPI; 2000-400052/34. (SCHW/) SCHWAB M E. (CHEN/) CHEN M S. Inhibitory-site WO200031235-A2 Modified-site Modified-site Modified-site Modified-site Modified-site Modified-site Modified-site 06-NOV-1998; 02-JUN-2000, Schwab ME, Rattus sp. Region Region Domain Domain Region

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Discognize to description of the CNS in disorders where neurite production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in disquosted screening methods for predisposition to disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. Note: The present sequence is not given in the specification but is derived from Nogo A protein sequence (AAY71310) and corresponds to residues 1-172 fused to 976-1163 of Nogo A. The specification claims an alternative version of this sequence (see AAY71385.) which corresponds to residues 1-172 fused to 975-1163 of Nogo A. SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in disclosure of the specification. However the specification does
   acids can be used to inhibit
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   Ribozymes or antisense Nogo nucleic
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Sequence 360 AA;

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Pred. No. 3e-65;
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neurotransmitter receptor protein Nogo-B. ABB81076 standard; protein; 360 05-NOV-2002 (first entry) ABB81076; ABB81076 RESULT

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Nerve regeneration, neuroprotection, neuronal degeneration; CNS; PNS; central nervous system; peripheral nervous system; tranquillizer; Nogo; vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant; nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic; osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy; neurotransmitter receptor; rat; receptor

Rattus norvegicus

US2002072493-A1

13-JUN-2002

28-JUN-2001; 2001US-00893348

98IL-00124500 98WO-US014715 19-MAY-1998; 21-JUL-1998;

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The invention relates to promoting nerve regeneration or conferring neuroprotection and preventing or inhibiting neuronal degeneration in the central/peripheral nervous system (NS). The method involves administering NS-specific antigen, its analogue or its peptide, a nucleotide sequence the NS-specific antigen or its analogue or combinations. The method is useful for promoting nerve regeneration and preventing neuronal degeneration in central/peripheral nervous system from injury/disease, where the injury is spinal cord injury, blunt crown injury/disease, where the injury is spinal cord injury, blunt crown injury/disease, where the injury is spinal cord injury, blunt crown injury/disease, where the injury is spinal cord injury, blunt crown injury/disease, where the injury is spinal cord injury, blunt crown injury/disease, where the injury is spinal cord injury, blunt crown injury/disease or neoplasm. The disease results in a degenerative crown injury/disease or neoplasm. The disease is not an autoimmune disease or neoplasm. The disease is not autoimmune disease or neoplasm. The disease is not autoinfury in either gray or white matter or both. The disease is disease, facial nerve (Bell's) play, glaucoma, Huntington's chorea, amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and vitamin deficiency, intervertebral disc herniation, prion diseases such as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral creuropathy, chronic ataxic neuropathy, inland, postution or organophosphates), charcot-Marie-Tooth disease, ataxia anyloidosis, obstructive lung diseases, acromegaly, malabsorption creample of various drugs are cromegaly, malabsorption creample of various drugs (e.g., metronidazole) and toxins (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, rebries, complications of various drugs (e.g., metronidazole) and toxing disease, or lipoproteinenia. The present sequence represents the rat
                                                                                                                              Cohen IR, Beserman P, Mosonego A;
                                                                                                                                                                                                                                                                                  nerve regeneration and preventing neuronal degeneration in
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99US-00314161.
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Sequence 360 AA;

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                  ALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 360
                                                                                                                                                                                                                                                                                                              Rat; neurite growth inhibitor; Nogo B; neural cell; myelin; CNS; central nervous system; neoplastic disease; antiproliferative; glioma; antisense gene therapy; neuroblastoma; menagioma; retinoblastoma; degenerative nerve disease; Alzheimer's disease; Parkinson's disease; pyperproliferative disorder; benign dysproliferative disorder; benign dysproliferative disorder; diagnosis; psoriasis; tissue hypertrophy; neuronal regeneration; treatment; structural plasticity; screening.
                                       301 ALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31. .58
/note= "Acidic region"
173. .361
/note= "Corresponds to amino acids 975-1163 of Nogo A
protein (AAY71310)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
11. .17
11. .17
12. see a corresponds to amino acids 1-172 of Nogo protein shown in AAY71310"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174. .361
/note= "This region is common to Nogo A, B and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "Inhibits NIH 3T3 fibroblast spreading"
                                                                                                                                                                                                                                                                           Alternative version of rat neurite growth inhibitor Nogo B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .86. .221
|label= Transmembrane_domain
'note= "C-terminal hydrophobic region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      region'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1988. 1323
Tlabel= Transmembrane domain
note= "C-terminal hydrophobic
139. 1341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "Protein kinase C (PKC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Protein kinase C (PKC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "Casein kinase II site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "Asn is N-glycosylated'
                                                                                                                                                       AAY71385 standard; protein; 361 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0107446P
                                                                                                                                                                                                                                   02-NOV-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SCHW/) SCHWAB M (CHEN/) CHEN M S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inhibitory-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200031235-A2
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                301
                                                                                                                                                                                            AAY71385;
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The present sequence is an alternative version of rat Nogo B protein
which is a potent neural cell growth inhibitor and is free of all central
cc which is a potent neural cell growth inhibitor and is free of all central
cc nervous system (CNS) myelin material with which it is natively
cassociated. The Nogo B transcript arises as a result of alternative
splicing of Nogo gene. Nogo proteins and fragments displaying neurite
cc growth inhibitory activity are used in the treatment of neoplastic
cdisease of the CNS e.g. glioma, glioblastoma, medulloblastoma, acoustic
crennopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic
crentoma, oligodendroglioma, menagioma, neuroblastoma, acoustic
cc neuroma, oligodendroglioma, menagioma, neuroblastoma or retinoblastoma
and degenerative nerve diseases e.g. Alzheimer's and Parkinson's
cc diseases. Therapeutics which promote Nogo activity can be used to treat
cc or prevent hyperproliferative or benign dysproliferative disorders e.g.
cp coriasis and tissue hypertrophy. Nibozymes or antisense Nogo nucleic
cor prevent hypertrophy production of Nogo protein to induce
cc acids can be used to inhibit production of Nogo protein to induce
cc desired. The animal models can be used in diagnostic and screening
cor desired. The animal models can be used in diagnostic and screening
cc desired from Nogo A protein sequence (AAY71310) and corresponds to
cresidues 1-172 fused to 975-1163 of Nogo A. This sequence is an
creamed from Nogo B sequence (see AAY71383) described in
calternative version of the Nogo B sequence (see AAY71383) described in
calds (residues 976-1163) of Nogo A. SEQ ID numbers 35-42 are referred in
claim 32 and SEQ ID No; 29 in disclosure of the specification. However
cc the specification does not include sequences for these SEQ ID numbers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                        Nogo proteins and nucleic acids useful for treating neoplastic disorders of the central nervous system and inducing regeneration of neurons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 PFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMWVFTYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MEDIDQSSLVSSSTDSPPRPPRAFKYQFVTEPEDEEDEEDEEDEEDEELEVLERK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPEROPSWERSPAAPPAPSLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAAGISAAAVPPAAAAPLIDFSSDSVPPAPRGPIPAAPPAAPFRQPSWERSPAAPAPSIP
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                                                                                                                                                                                        Claim 4; Page; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 360; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
WPI; 2000-400052/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 361 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D 360
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Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS; central nervous system; neoplastic disease; antiproliferative; glioma; antisense gene therapy; neuroblastoma; menagioma; retinoblastoma; degenerative nerve disease; Alzheimer's disease; Parkinson's disease; hyperproliferative disorder; benign dysproliferative disorder; diagnosis; psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
                                                              FRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVD 300
  181 AASEPVIPSSAVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 240
                                                                                                                                             301 DLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHOVQIDHYLGLANKSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSV
                                         FRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172. .259 /
/note= "This region is not essential for inhibitory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Region specifically described in claim 16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "Inhibits NIH 3T3 fibroblast spreading"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gite"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "Protein kinase C (PKC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "Protein kinase C (PKC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "Protein kinase C (PKC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "Protein kinase C (PKC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "Casein kinase II site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242. .244
/note= "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PKC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "Protein kinase C (PKC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "Protein kinase C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "Casein kinase II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "Encoded by TTG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Acidic region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rat neurite growth inhibitor Nogo A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1. .171
                                                                                                                                                                                                                                                                                                                                         AAY71310 standard; protein; 1163 AA
                                                                                                                                                                                                   KDAMAKIQAKIPGLKRKAD 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          structural plasticity; screening
                                                                                                                                                                                                                                       KDAMAKIQAKIPGLKRKAD 379
                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                activity"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31. .57
/note= "F
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of gene sequence that is down-regulated in response to streptozocin-
induced diabetes, vector, host cell, animal, polypeptide and antibody, in
screening of compounds for treating or diagnosing pain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           regulated in the spinal cord in response to streptozocin-induced diabetes, or comprising, hybridising or having at least 80% sequence by the sequence whose expression products are kinases, phosphatases, ion channel proteins, receptors, transporters, G-protein coupled receptor proteins, DNA-binding proteins, proteases or enzymes, given in the specification. A gene of the invention has analgesic activity, and may have a use in gene therapy. The gene sequences, vector, host cell, animal, polypeptide and antibody are useful for screening of compounds for diagnosing or treating pain. The kits are useful for simultaneous, separate or sequential detecting and/or quantifying downergulation of a gene sequence in the spinal cord of a mammal in response to streptozocin-induced diabetes. The compound or pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAFLP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        composition is useful as a medicament for treating or diagnosing pain. The present sequence represents a protein encoded by a gene of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTBPEDEEEEEBEEEBEBDBDLEELEVLERK
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                                                                                                                                                        rat; streptozocin; kinase; phosphatase; ion channel protein; recepto; transporter; G-protein coupled receptor; GPCR; DNA-binding proteins; protease; enzyme; analgesic; gene therapy; pain; diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention relates to a novel isolated gene sequence that is down-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 7; Length 379;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 99.2%; Score 1808.1; DB 7; Best Local Similarity 94.7%; Pred. No. 7.5e-65; Matches 359; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pinnock RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 239-240; 256pp; English.
                                                                                                                    Rat foocen-m2 reticulon SEQ ID NO:164.
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standard; protein; 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lee
                                                                                                                                                                                                                                                                                                                                                            26-JUL-2002; 2002EP-00255228.
                                                                                                                                                                                                                                                                                                                                                                                                 27-JUL-2001; 2001GB-00018354.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (WARN ) WARNER LAMBERT CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dixon AK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-364994/35.
N-PSDB; ADB85284.
                                                                                                                                                                                                                                         Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 379 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brooksbank RA,
                                                                                                                                                                                                                                                                            EP1284297-A2
                                                                             04-DEC-2003
                                                                                                                                                                                                                                                                                                                      19-FEB-2003.
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                                     ADB85283;
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ADB85283
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The present sequence is a rat Nogo A protein which is a potent neural cell growth inhibitor and is free of all central nervous system (CNS) wyelin material with which it is natively associated. The protein was derived from a cDNA generated by fusing R018037-3, R1-3021 cDNAs isolated from hexanucleotides-primed rat brain stem/spinal cord library, and Oli18 comparation oligo d(T)-primed rat oligodendrocyte library. Nogo proteins and fragments displaying neutre growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, cranipharyngioma, ependyoma, pinelona, menagioma, haemangioblastoma, cranipharyngioma, oligodendroglioma, menagioma, chamangioblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regentation of neurons or to production of Nogo protein to induce regentation of neurons or to product can be used in diseases of the CNS in disorders where neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in diseases of the CNS in the sequence squence of esignated as SEQ ID NO: 2 is stated to be the same as the sequence of designated as SEQ ID NO: 2 is stated to be the same as the sequence of efferted in claim 32 and SEQ ID NO: 29 in disclosure of the sequence for the sequence given in Fig. 13 (see AAY71384) of the specification does not include sequences for the second of the sequence of the second of the sequence of the second of the sequence of the second of the sequence of the second of the sequence of the second of the sequence of the second of the sequence of the second of the sequence of the second of the sequence of the second of the second of the sequence of the second of the second of the second o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 GNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSSFKGSPKGES 300
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  the central nervous system and inducing regeneration of neurons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels 803;
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Pred. No. 5.7e-61;
0; Mismatches 0
                                                  Claim 3; Fig 2A; 122pp; English.
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31.0%;
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Matches 360; Conservative
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                                                                                                                                             note= "used as immunogen to generate antibody AS Bruna"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "This region is not essential for inhibitory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            988. .1023
/Jabel= Transmembrane_domain
/note= "C-terminal hydrophobic region specifically
described in claim 16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= Transmembrane domain
/note= "C-terminal hydrophobic region specifically
described in claim 16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "PKC and casein kinase. II sites"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "PKC and casein kinase II sites"
'note= "Protein kinase C (PKC) site"
                                                                                                                                                                                             note= "Protein kinase C (PKC) site"
                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "Protein kinase C (PKC) site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "Protein kinase C (PKC)
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                                                                                                                                                                                                                                                                                                                                                                                          note= "Casein kinase II site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "Asn is N-glycosylated"
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                                               'note= "Asn is N-glycosylated"
                                                                                             note= "Casein kinase II site"
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note= "Asn is N-glycosylated"
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note= "used as immunogen to generate antibody AS Bruna"
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                                                              Leu at this position in the sequence
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172. .259
/note= "This region is not essential for inhibitory
                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "used as immunogen to generate antibody
                                                                                                                                                                                                                                                                                          /label= Unknown
/note= "There is Lys at this position in the
shown in AAY71310"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "PKC and casein kinase II sites"
956
/note= "PKC and casein kinase II sites"
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/note= "Asn is N-glycosylated"
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note= "Asn is N-glycosylated"
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                                                            /note= "There is L
shown in AAY71310"
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                                                  label= Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS; central nervous system; neoplastic disease; antiproliferative; glioma; antisense gene therapy; neuroblastoma; menagioma; retinoblastoma; degenerative nerve disease; Alzheimer's disease; Parkinson's disease; pyperproliferative disorder; benign dysproliferative disorder; benign dysproliferative disorder; benign dysproliferative disorder; benign sproliferative disorder; benign structural plasticity; screening.
                                                                                                                                                                                                                                                                                          841 IIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK 900
                                                                                                                                     661 NAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESE
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                                   NEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSL
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'note= "Inhibits NIH 3T3 fibroblast spreading"
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/note= "Acidic region"
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) in disclosure of the specification. However the specification include sequences for these SEQ ID numbers
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(CHEN/) CHEN M S.
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                                                   1 MEDIDQSSLVSSSTDSPPRPPAFKYQFVTEPEDEEDEEBEBEBEBEBEBELBELEVLERK
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                                                                                                                                     PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is an alternative version of rat Nogo A protein which is a potent neural cell growth inhibitor and is free of all central nervous system (CNS) myelin material with which it is natively associated. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, haemangioblastcoma, caniopharyngioma, cpendyoma, pinealoma, haemangioblastcoma, coustic neuroma, clionaciona, haemangioblastcoma or retinoblastcoma and capenarative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative or benign dysproliferative disorders e.g. psoriasis and tiseale hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where neurons or to promote structural plasticity of the CNS in disorders where on inhibit respectation or maintenance are deficient or desired. The animal models can be used in diagnostic and screening methods for predisposition to disorders and to screen for or test molecules which can cape or prevent disorders and to screen for or test molecules which can be used in diagnostic and screening methods for creat or prevent disorders and to screen for or test molecules which can be an alternative version of the Nogo A sequence shown in Fig. 20 (see AAY71310). SEQ ID numbers 35-42 are referred in claim 32 and 52 and 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nogo proteins and nucleic acids useful for treating neoplastic disorders of the central nervous system and inducing regeneration of neurons.
                                                                                                      and
                                                                                                   note= "C-terminal common region found in Nogo A, B
"This region is not essential for inhibitory
                                                                                                                                                                 88. .1023
label= Transmembrane domain
note= "C-terminal hydrophobic region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     090. .1125
|abel= Transmembrane_domain
note= "C-terminal hydrophobic region"
                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "Protein kinase C (PKC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "Protein kinase C (PKC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "Asn is N-glycosylated'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Fig 13; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-US026160,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0107446P.
                                                                 . .1163
                           activity"
                                                                                                                                  вототов
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1020

277

960

900

171

171

1;

Gaps

95.0%; Score 1732.7; DB 3; Length 1163; 31.0%; Pred. No. 5.7e-61; ive 0; Mismatches 0; Indels 803;

Best Local Similarity 31.0 Matches 360; Conservative

VTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL

961 RSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS

---SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS

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901 DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKED

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The invention relates to promoting nerve regeneration or conferring neuroprotection and preventing or inhibiting neuronal degeneration in the central/peripheral nervous system (NS). The method involves administering NS-specific antigen, its analogue or its peptide, a nucleotide sequence the NS-specific antigen or its analogue or combinations. The method is useful for promoting nerve regeneration and preventing neuronal degeneration in central/peripheral nervous system from injury/disease, where the injury is spinal cord injury, blunt frauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or damages caused by surgery such as tumour excision. The disease is not autoimmune disease or neoplasm. The disease results in a degenerative concimmune disease or neoplasm. The disease results in a degenerative cliabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea, amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and vitamin deficiency, intervertebral diseases, including but not limited neuropathies associated with various diseases, including but not limited
Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS; central nervous system; tranquillizer; Nogo; vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant; noctropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic; osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mosonego A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neurotransmitter receptor protein Nogo-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neurotransmitter receptor; rat; receptor
                                                                                                                                                                   Example 5; Page 44-47; 93pp; English.
                                                                                                                                 NKSVKDAMAKIQAKIPGLKRKAD 360
                                                                                                                                                                                                                                                                                                                                                               ABB81074 standard; protein; 1163 AA
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98WO-US014715.
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sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary amyloidosis, obstructive lung diseases, acromegaly, malabsorption syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-pathies, complications of various drugs (e.g., metronidazole) and toxins (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia adrenomyeloneuropathy, Giant axonal neuropathy, Refoun's disease, Fabry's disease, or lipoproteinemia. The present sequence represents the rat neurotransmitter receptor protein Nogo-A, an example of NS-specific
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                                                                                                                                                                                                         Length 1163;
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Pred. No. 5.7e-61;
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31.0%;
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Matches 360;
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PAAAVLPSKLPEDDEPPARPPPPPAGASPLAEPAAPPSTPAAPKRGSGS------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New binding molecule that binds to the human NogoA polypeptide, NiG, NiG-D20 or NogoA623-640, useful in preparing a composition for treating CNS injury or neurodegenerative disorders.
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                                                                                                                                                                                                                                                                                                                                                                                      binding molecule; human; NogoA; NiG; NiG-D20; NogoA_623-640;
nerve repair; neuroprotective; gene therapy;
central nervous system injury; CNS injury; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEDEEBEBEBEBEBEDDEDLEELEVLERK
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                                                                                                                                                                               ADP45572 standard; protein; 1163
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(NOVS ) NOVARTIS PHARMA GMBH.
(UYZU-) UNIV ZUERICH.
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Zurini M;
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Rat, neurite growth inhibitor; Nogo A; neural cell; myelin; CNS; central nervous system; neoplastic disease; antiproliferative; glioma; antisense gene therapy; neuroblastoma; menagioma; retinoblastoma; degenerative nerve disease; Alzheimer's disease; Parkinson's disease; hyperproliferative disorder; benign dysproliferative disorder; diagnosis; psoriasis; tissue hypertrophy; neuronal regeneration; treatment; structural plasticity; screening; mutant; mutein.
                                                                    Nogo A truncated protein used in the construction of mutant Nogo-A.
                 AAY71557 standard; protein; 1162 AA
                                                                                                                                                                                                          99WO-US026160
                                                                                                                                                                                                                         06-NOV-1998; 98US-0107446P
                                                  02-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                   Chen MS;
                                                                                                                                                                                                                                                                                    WPI; 2000-400052/34
                                                                                                                                                                                                                                          (SCHW/) SCHWAB M E. (CHEN/) CHEN M S.
                                                                                                                                                                       WO200031235-A2
                                                                                                                                                                                                        05-NOV-1999;
                                                                                                                                                                                                                                                                   Schwab ME,
                                                                                                                                                       Rattus sp.
                                  AAY71557;
RESULT 11
AAY71557
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Nogo proteins and nucleic acids useful for treating neoplastic disorders of the central nervous system and inducing regeneration of neurons.

Example; Page; 122pp; English.

The patent relates to neurite growth inhibitor Nogo which is free of all central nervous system (CNS) myelin material with which it is natively central nervous system (CNS) myelin material with which it is natively central nervous system (CNS) myelin material with which it is natively cansociated. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, haemangloblastoma, acoustic neuroma, coligodendroglioma, nenagioma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.

CC Therapeutics which promote Nogo activity can be used to treat or prevent hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where constructing growth, regeneration or maintenance are deficient or desired. The neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in diagnostic and screening methods for prevent disorders or diseases of the CNS. The present sequence treat or prevent disorders or diseases of the CNS. The present sequence creation of matent Nogo-A sequence from animo acids 172-974, cased for mapping the inhibitory sites of Nogo protein. Major inhibitory credion was identified in the Nogo A sequence from amino acids 542-722. In addition, N. terminal region 1-171 was found to be inhibitory to NIH 373 fibroblast spreading. Note: The was found to be inhibitory to NIH 373 fibroblast spreading. Note: The was found to be inhibitory to NIH 373 fibroblast spreading. Note: The Numbers and Sequence shown in AAY1310. SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in disclosure of the specification.

Sequence 1162 AA;

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                                                                                                                                          561 NAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSBIAKFEKSVPEHAELVEDSSPESE
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Length 1162;
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 Score 1726.7;
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                 Best Local Similarity 30.9
Matches 359; Conservative
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                                                                         337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Regenerating nerves or modulating nerve regeneration comprises inhibiting or modulating p75 signal transduction pathway by administering a transduction agent, e.g. p21 or Rho, or an agent that interacts with the transduction agent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a method for regenerating nerves or modulating nerve regeneration. The method involves inhibiting or modulating a p75 signal transduction pathway. The invention is useful for treating, preventing or diagnosing neurological diseases based on nerve regeneration and for identifying agents useful for nerve regeneration. The invention is also useful in gene therapy and for preparing vaccine. The present sequence is the Mus musculus Nogo protein. Note: This sequence is said to encoded by SEQ ID NO 9, however this does not appear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                    FLVDDLVDSLKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              regeneration; gene therapy; vaccine; neuroprotective; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEDEEEEBDEEEDDEDLEELEVLERK
                                                                       FLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLA
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Pred. No. 4.2e-57;
2; Mismatches 6; Indels 810.
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                                                                                                                                                                 NKSVKDAMAKIQAKIPGLKRKA 359
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30-APR-2003; 2003US-00427741.
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N-PSDB; ADT89536.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a method of identifying compounds that influence fat cell number or size comprising providing a cell that expresses a gene and an agent, exposing the cell to the agent and identifying fat cell number or size relative to cells not exposed to the agent. The method also comprises providing an expression vector and an agent, exposing the vector to the agent, detecting a charge in expression of the gene relative to expression of the gene in an expression of the gene crative to expression of the agent and agent, treating a subject with the agent and identifying fat cell number or size in the subject with the agent comprises an antistense chigonucleotide. The subject comprises a manishan and agent, exposing the polypeptide to the agent, detecting binding of the agent to the gubject with the agent and identifying fat cell number or size in the subject. The agent and identifying fat cell number or size in the subject. The agent and identifying fat cell number or size in the subject. The agent and identifying the method of regulating fat cell number or size in the subject. The agent and identifying the method of regulating fat cell number or size in the subject. The agent and identifying the method of regulating fat cell number or size in the subject. The agent and adentifying the method of regulating fat cell number or size in the subject. The agent and adentifying the method of regulating fat cell number or size in the subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying compounds that influence fat cell number or size for treating or preventing obesity or diabetes by exposing the cell to the agent and identifying fat cell number or size relative to cells not exposed to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    number or size comprises providing a subject containing fat cells and an agent that changes the expression of a gene, and treating the subject with the agent under conditions so that fat cell size or number in the subject is altered. The method is useful for identifying compounds that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              influence fat cell number or size, for preparing a composition for treating or preventing obesity or diabetes. This sequence represents a mouse polypeptide used in the scope of the invention.
                                                                                                                                                                                    Mouse; fat cell number; fat cell size; obesity; diabetes; anorectic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tch 89.0%; Score 1622.9; DB 8; Length 1163; al Similarity 29.7%; Pred. No. 1.6e-56; 347; Conservative 2; Mismatches 7; Indels 811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 14; SEQ ID NO 431; 275pp; English.
                                  AD008105 standard; protein; 1163 AA
                                                                                                                                                                                                                                                                                                                                                        09-OCT-2002; 2002US-00267502.
                                                                                                                                                                                                                                                                                                                                                                                         09-OCT-2002; 2002US-00267502.
                                                                                                                                                Mouse polypeptide #57
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N-PSDB; ADO07888.
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                                                                                                                                 119 PAAAVLPSKLPEDDEPPAR--PPAPAGASPLAEPAAPPSTPAAPKRGSGSVDETLFALP
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9

Gaps

17;

20;

; Pred. No. 1.4e-56; 11; Mismatches 20

87.9%; Score 1603.3;

87.28;

Query Match Best Local Similarity 87.29

Sequence 373 AA;

DB 3; Length 373; Indels ၀ 28 59 PAAGESAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVP 118

116 APSLPPAAAVLPSKLPEDDEPPARPPPPAGASPLAE------PAAPPSTPAAPKR 166

119 APSPLSAAAVSPSKLPEDDEPPARPPPPPASVSPQAEPVWTPPAAPAAPPSTPAAPKR

PAAGLSAAAVP--PAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA--P 115

61

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셤 ò

1 MEDLIQSPLVSSS-DSPPRPQPAFKYQFVREPEDEBE-EBEBEBEBEBDEDLEBLEVLERK 1 MEDIDOSSLVSSSTDSPPRPPARKYQFVTEPEDBEDBEBEBEBEDBEDLEBLEVLERK

178

225

285

179 RGSSGSVVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIY 238

RG-SGSSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAY1ALALLSVTISFRIY

167

239 KGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVD 298

KGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVD

226

286 299

SLKFAVLMWVFTYVGALFNGLFLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAM 358 SIKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAM 345

AAY56969 standard; protein; 373 AA.

RESULT 15 AAY56969

AAY56969;

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Bone marrow secreted protein, bone marrow stromal cell; cytokine; cell proliferation; cell differentiation; hematopoiesis; anaemia; myeloid cell deficiency; lymphoid cell deficiency; myeloid cell; merythroid progenitor cell; colony stimulating factor; granulocyte; monocyte; macrophage; myelo-suppression; megakaryocyte; platelet disorder; thrombocytopenia; hematopoeitic stem cell; stem cell disorder; aplastic anaemia; bone differentiation; paroxysmal nocturnal hemoglobinuria; bone growth; cartilage; tendon; bone fracture; cartilage damage; artificial joint.
                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated human polynucleotide and secreted proteins can induce production of other cytokines in certain cell populations.
                                                                                                              A bone marrow secreted protein designated BMS112
1137 LGLANKSVKDAMAKIQAKIPGLKRKAE 1163
                                                 AAY53624 standard; protein; 373
                                                                                                                                                                                                                                                                                                                                           98US-0101603P.
98US-0102540P.
                                                                                                                                                                                                                                                                                                              98WO-US027008
                                                                                                                                                                                                                                                                                                                                  97US-0068958P
                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-038344/03.
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                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAZ36230
                                                                                                                                                                                                                                                                                                                                                                                               Cao L;
                                                                                          22-FEB-2000
                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                     WO9933979-A2
                                                                                                                                                                                                                                                                                                              18-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                     30-SEP-1998;
                                                                                                                                                                                                                                                                                                                                  30-DEC-1997;
                                                                                                                                                                                                                                                                                                                                             24-SEP-1998;
                                                                                                                                                                                                                                                                                         08-JUL-1999
                                                                     AAY53624;
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                             RESULT 14
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SMIK ) SMITHKLINE BEECHAM PLC
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99GB-00016898.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAZ56888.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Michalovich D,
                                                                                                                                                                                                                                                                                                                                                                                        WO200005364-A1
                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                           03-FEB-2000,
cell differentiation activity (either inducing or inhibiting). They can be used to support colony forming cells or factor-dependent cell lines, to requiste hematopoissis, and to treat myeloid or lymphoid cell inse, to requiste hematopoissis, and to treat myeloid or lymphoid cell lines, to requiste hematopoissis, and to treat myeloid or lymphoid cell lines, to requiste hematopoissis, and to treat myeloid cell such as proliferation of erythroid progenitor cells, and to treat various anaemias. They can have colony stimulating factor (GSF) activity and can be used to support the growth and proliferation of myeloid cells such as granulocytes, monocytes or macrophages, to prevent or treat myelocoupport to support the growth and proliferation of myeloid cells such as and platelets, thereby allowing prevention or treatment of platelet conjunction with platelet transfusions, to treat stem cell disorders, conjunction with platelet transfusions, to treat stem cell disorders, such as aplastic anaemia and parcysmal nocurnal hemoglobinuria, or to repopulate the stem cell compartment after irradiation or chemotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     They can be used for growth or differentiation of bone, cartilage, tendon, ligament, or nerve tissue, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers, to induce cartilage and/or bone growth in circumstances where bone is not normally formed and thus have an application in healing bone
                                                                                                                                                                                                                                                                                  AAY53622-43 represent bone marrow secreted proteins of human bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fractures and cartilage damage or defects, prophylactic use in fracture reduction and also in the improved fixation of artificial joints
                                                                                                                                                                                                                            Claim 2; Page 74; 120pp; English
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MAGI protein; neuroendocrine-specific protein; neuropathy; human; spinal injury; neuronal degeneration; neuromascular disorder; cancer; psychiatric disorder; developmental disorder; inflammatory disorder; africke; cytostatic; cerebroprotective; neuroprotective; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel polypeptides related to neuroendocrine-specific proteins and polynucleotides useful for diagnosis of various diseases and for treatment of cancer and neurological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Page 22; 35pp; English
                                                                                             Human MAGI polypeptide variant.
(first entry)
    25-APR-2000
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us-09-830-972-2-fused.rag

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61 PAAGLSAAAVP--PAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P 115
                                                                                                                                                                                                                                                                                                                                                                   PAAGLSAAPVPTAPAAGAPLMDFGNDFVPFAPRGPLPAAPPVAPĘRQPSWDPSPVSSTVP 118
                                                                                                                                                                                                                                                                                                                                                                                                                   166
                                                                                                                                                                                                                                                                                                                                                                                                                                     RG-SGSSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIY 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVD 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAM 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to human MAGI protein, which is similar to neuroendocrine-specific protein. The MAGI protein can be expressed by standard recombinant methodology. The MAGI polypeptides, polynucleotides and antibodies are useful for treating diseases, including neuropathies, spinal injury, neuronal degeneration, neuromuscular disorders, psychiatric disorders and developmental disorders, cancer, stroke and inflammatory disorders. The polynucleoitde is also useful for chromosome localization and for tissue expression studies. The present sequence represents the human MAGI protein variant
                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                APSLPPAAAVLPSKLPEDDEPPARPPPPAGASPLAE------PAAPPSTPAAPKR
                                                                                                                                                                                                                                                                                 MEDIDQSSLVSSSTDSPPRPPAFKYQFVTEPEDEEDEEEEEDEEDDEDLEELEVLERK
                                                                                                                                                                                                                                                20; Indels 17; Gaps
                                                                                                                                                                                                             ; Score 1603.3; DB 3; Length 373; ; Pred. No. 1.4e-56; 11; Mismatches 20; Indels 17;
                                                                                                                                                                                                                87.9%;
87.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AKIQAKIPGLKRKAD 360
                                                                                                                                                                                                             Query Match
Best Local Similarity 87.2%
Matches 327, Conservative
                                                                                                                                                                                 Sequence 373 AA;
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Search completed: June 23, 2005, 10:52:00 Job time : 119.842 secs

359 AKIQAKIPGLKRKAE 373

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GenCore version 5.1.6

Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 23, 2005, 10:29:31; Search time 24.9653 Seconds (without alignments)

1387.446 Million cell updates/sec

Perfect score: 1823
Sequence: 1 MEDIDQSSLVSSSTDSPPRP......VKDAMAKIQAKIPGLKRKAD 360

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.1
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Total number of hits satisfying chosen parameters: 283416

283416 seqs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database: PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	neuroendocrine-spe	neuroendocrine-spe	tropomyosin-relate	hypothetical prote			ne	C-terminal domain-	hypothetical prote	cappuccino gene pr	끆	-	unconventional myo	formin - mouse	hypothetical prote		hypothetical prote	diaphanous protein	proline-rich prote	unknown protein (i	DNA topoisomerase		hypothetical prote	н	hypothetical prote		unconventional myo	hypothetical prote	FREAC-4 - human
SUMMARIES	ΙD	A46583	160904	A60021	T26216	T26215	T26213	A35466	T31421	T38236	T13286	JC8033	S24407	A59266	S11515	T26998	F86387	C96623	T31065	S71461	G86441	JC6552	E96636	T19536	T39371	A71416	EDBEIF	A59295	\sim	G02738
	DB	7	7	~	7	~	~	~	~	7	~	7	7	~	~	~	~	~	~	N	7	~	~	7	7	~	-	~	~	7
	Length	776	208	267	2484	2607	222	786	1173	1611	1058	1100	1206	3530	1468	716	760	929	1255	2157	1201	1015	907	1657	1522	645	1460	3511	710	465
dł	Query	45.3	37.5	36.7	24.0	23.4	18.5	14.9	14.6	14.6	14.2	14.1	14.1	14.1	14.0	14.0	13.9	13.9	13.9	13.8	13.8	13.8			•	٠	13.5	13.5	13.4	13.4
	Score	826.3	683	699	437.7	27.	337.5	72.	. 99	65.	58.	57.	257.5	26.	54.	254.7	53.	253.2	253.2	252.2	251.9	250.9	250.2	246.4	246	245.8	245.4	245.2	245.1	244.7
	Result No.		8	٣	4	5	9	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

formin related pro	hypothetical prote	serine/proline-ric	Bassoon protein -	immediate-early pr	probable cell divi	hypothetical prote	immediate-early pr	hypothetical prote	masquerade precure	probable cytoskele	elastic titin - hu	BPLF1 protein - hu	progesterone recep	regulatory protein
T13963	S48375	A58198	T42761	EDBE11	G75523	T26517	A45344	T04455	A55617	T37781	I38346	QQBE8	QRHUP	S54986
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.,.	13.3	13.3	13.3	13.2	13.2	13.2	13.2	13.1	13.1	13.1	13.1	13.1	13.0	13.0

ALIGNMENTS

RESU	RESULT 1	
A46583	A46583 neuroendocrine-specific protèin. splice form A – human	
S, C	fic protein, spli	
10.00 10.00	C.Date: 24. Mon. Obj. C. M. C. C. Date: 24. May-1996 #text_change 09-Jul-2004	
R;Ro	R;Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers,	kers, F.C.; Va
J. B	J. Biol. Chem. 268, 13439-13447, 1993 A,Title: Cloning and expression of alternative transcripts of a novel neuro	neuroendocrine-spec
A;Re	A;Reference number: A46583; MUID:93293865; PMID:7685762 A;Accession: A46583	
A;St A:Mo	A;Status: preliminary; translated from GB/EMBL/DDBJ A:Molecule type: mRNA	
A;Re	A, Regidues: 1-776 < ROSI>	
A; Ac	A;cross-rerences: Unifru:Qib/39; GB:Liu333; Nil;g30/305; Film:AAA59950.1; A;Accession: I60903	; F1D:g30/30/
A;St	A;Status: preliminary; translated from GB/EMBL/DDBJ	
A;Re	A; Residues: 421-776 (ROE2>	
A C	A;Cross-rererences: GB:LIU334; NID:g307308; FIDN:AAA5995I.1; FID:g307309 C:Genetics:	
A A G	A.Gene: GDB:RTN1; NSP A.Cross-references: GDB:203968; OMIM:600865	
A; Wa	A;Map position: 14q21-14q22	
86	Query Match 45.3%; Score 826.3; DB 2; Length 776;	
Ma	ative 52	17;
ò	10 VSSTDS	19
đ	: 85 VSSAMDHTFSTTSKDGEGSCYTSLISDICYPPQEDSTYFTGILQKENGHVTISESPEELG	144
ò	20 - PPPAPKYQFVTEPED	34
đ		204
ò	35 BEDEBERBEDEREDDED	50
qq	1	264
ò	51	55
a	1: 265 DDLSBEQRRAPQITTPVKITLTBIBPSVETTTQEKTPEKQDICLKPSPDTVPTVTVSEPË	324
ò	56	99
g G	325 DDSPGSITPPSSGTEPSAAESQGKGSISEDELITAIKEAKGLSYETAENPRPVGQLADRP	384
δ	67 PAAVPPAAAAPLLDFSSDSV	89

us-09-830-972-2-fused.rpr

Db 385 EVKARSGPPTIPSP-LDHEASSAESGDSEIELVSEDPMAAEDALPSGYVSFGHVGGPPPS 443 Qy PRGPL	C;Accession: A60021 R;Wieczorek, D.F.; Hughes, S.R. Brain Res. Mol. Brain Res. 10, 33-41, 1991 Brain Res. Mol. Brain Res. 10, 33-41, 1991 A;Title: Developmentally regulated cDNA expressed exclusively in neural tissue. A;Reference number: A60021; MUID:91278684; PMID:1647480 A;Accession: A60021 A;Accession: A60021 A;Accession: A60021 A;Accession: Basidues: 1-267 cWIE> A;Accession: A60021 A;Accession: Basidues: 1-267 cWIE> A;Cross-references: EMBL:X52817; NID:9456549; PIDN:CAA37001.1; PID:9456550 C;Comment: This neuronal-specific mRNA was identified by hybridization to an alpha-tropon Query Match Best Local Similarity 66.7%; Pred. No. 1e-15; Matches 124; Conservative 32; Mismatches 30; Indels 0; Gaps 0; A SSYUDLLYMRDIKKTGVPGASLFLLSITVFSIVSVTAYIALALSVTISFRIYKGVIQ 69 CY 171 SGVUDLLYMRDIKKTGVPGASLFLLSITVFSIVSVTAYIALALSVTISFRIYKGVIQ 69 CY 231 AIQKSDEGHPFRAYLESEVAISBELVQKYSNSALGHVNSTIKELRRLFLVQDLVDSLKFA 290 A 231 AIQKSDEGHPFRAYLESEVAISBELVQKYSNSALGHVNSTIKELRRLFLVQDLVDSLKFA 290 A 231 AIQKSDEGHPFRAYLELBITLSQEQIQKYTDCLQLYVNSTIKELRRLFLVQDLVDSLKFA 290 B 70 AVQKTDEGHPFRAYLELBITLSQEQIQKYTDCLQLYVNSTIKELRRLFLVQDLVDSLKFA 129 CY 291 VLAWWLIYYCALPRGITLLIALISLESIPVIYERHQVQIDHYCGLANKSVKDAMAKIQA 350 A 291 VLAWLLTYVGALPRGITLLLALISLESIPVIYERHQVQIDHYCGLANKSVKDAMAKIQA 189 A 291 VLAWLLTYVGALPRGITLLLLALISLESIPVIYERHQVQIDHYCGLANTHINTVVAKIQA 189
RESULT 2 IG0904 neuroendocrine-specific protein C - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004 C;Accession: IG0904 R;Roebrock, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; V R;Roebrock, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; V R;Roebrock, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; V R;Roebrock, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; V A;Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-spe A;Accession: IG0904 A;Accession: IG0904 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Rolecule 'Type: mRNA A;Residues: 1-208 -RES> A;Cross-references: UNIPROT:Q16799; GB:L10335; NID:g307310; PIDN:AAAS9952.1; PID:g307311 C;Genetics: GDB:RTN1; NSP A;Genetics: GDB:RTN1; NSP A;Genetics: GDB:203968; OMIM:600865 A;Map position: 14q21-14q22	Qy 351 KIPGLK 356 Db 190 KIPGAR 195 RESULT 4 T26216 Tyberical protein W06A7.3c - Caenorhabditis elegans C;Species: Caenorhabditis elegans
Query Match Best Local S Matches 128 171	A;Axbeliantial Boutce: Cloud Work) C;Genetian: A;Genetian: A;Genetian: A;Genetian: A;Genetian: A;Map position:
Qy 231 AIOKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNATIKELRRLFIUVDLVDSLKFA 290 - - - - - - - - - -	MEDIDQSSLVSSST
RESULT 3 A60021 tropomyosin-related protein, neuronal - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 05-Nov-1999	Qy 45

אור 1000 אינויי בחימויאיסארטים מיבירט בחימוי מרבירט בחימוי אורי אורי אורי אורי אורי אורי אורי או		
1000 SECHDSTEDINGERITÄRFNISTDDFSIRKDSFSSISSFGDRÜKFKIAIE		-
Qy 58	63 Qy	15DSPPRPPPAFKYQFVTEPEDE
Db 1866 SVSQYLRSSPNPSQQLLVTNLSMDSPSDLSPNAPPVGFENTAQFLEKLQQEDRPSAEGSI	ISI 1925 Db	1626 EQAPTIPQRPPRAPKSELPKVAKPLDDSKSRVRFAPLNIKLGRTYSEEQQKELVESLERP 1685
Oy 64GLSAAAVPP	72 Oy	36BEBEBDB 44
Db 1926 DSSGFEKVDHEGLDEFAAPPVHDPMQKSVFGSLGSDDMKPGSQDDGFVFIERNEANEATL	TL 1985 Db	1686 LTIITQQKPPEKPTEDIGALSPNTLAEYEEVPMMDMQSVPHSPQEKQEBIEALSEII 1745
Oy 73	79 Qy	4557
Db 1986 KKNQKMSSHHNDVIEKNYFNDNAPTAALLESPIAEEARKLVQDAVESASEYKKQAVDSGD	GD 2045 Db	1746 BEPQAMKEVEKPVESAPEKDNESLEAPEIINEPIRRVLVETKIMGPGKSLNEDNDDDDDG 1805
Qy 80PRGPL	PL 94 Oy	58 57
Db 2046 BIGRELLDNVEQKIEQVKEPIVDSLHKAYDGVGDFVHETVPNAVDDFVREAEKQLPESPV	: PV 2105 Db	1806 SECLDSIGDLSERTIQRFNTSIDDPSIRRDSFSSISSFGDRQKFRTAIENIRQDLLPFQS 1865
Qy 95 PBRQ	RQ 105 OY	58
Db 2106 PEKIETPEPLVDIHDTVDKVHDEVDNFLRREPTPPFETDDVAPLSDDKPQFGNQTPEEDE	DE 2165 Db	1866 SVSQYLRSSPNPSQQLLVTNLSMDSPSDLSPNAPPVGFENTAQFLEKLQQEDRPSAEGSI 1925
Qy 106 PSWERSPAAPABLPPAAAVLPSKLPEDD	DD 134 QY	64
Db 2166 TTFDRKGPLTIPEEVEKAAAAQNNDLDDFDPLVTSNTGAAFGAAVGAAAAVESLTEEE	BE 2223 Db	1926 DSSGFEKVDHEGLDEFAAPPVHDPMQKSVFGSLGSDDMKPGSQDDGFVFIERNEANEATL 1985
Qy 135FRPPPPPAGASPLAEPAAPPSTPAAPKRRGSG-	G- 170 Qy	73 AAAAPLII 79
Db 2224 MFGHQKFETVPRPPTPPKDISDEDVKPSTVNLGPSHHHSHPSSPHHSILKHHGDAW	AW 2279 Db	1986 KKNQKMSSHHNDVIEKNYFNDNAPTAALLESPIAEEARKLVQDAVESASEYKKQAVDSGD 2045
Qy 171SSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFR	FR 223 Oy	80
Db 2280 IDFKTVPPCVLDVIYWRDAKKSAIVLSLALLVLFVLAKYPLLTVVTYSLLLALGAAAGFR		2046 BIGRELLDNVEQKIEQVKEPIVDSLHKAYDGVGDFVHETVPNAVDDFVREAEKQLPESPV 2105
Qy 224 IYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDL	DL 283 QY	95 PBRQ 105
Db 2340 VFKKVEAQİKKTDSEHPFSEILAQDLTLPQEK'HAQADVFVEHATCIANKLKKLVFVESP	SP 2399 Db	2106 PEKIETPEPLVDIHDTVDKVHDBVDNFLRREPTPFFETDDVAPLSDDKPQFGNQTPEEDE 2165
Qy 284 VDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKD	343	
Db 2400 LESIKFGLVLWSLTYIASWFSGFTLAILGLLGVFSVPKVYESNQEAIDPHLATISGHLKN	KN 2459 Db	2166 TTFDŘKGPLTIPEEVEKAAAAQNNDLDDFDPLVTSNTGÄÁFGAAVGAÄÄÄVESĽTEEE 2223
Qy 344 AMAKIQAKIPGLK 356 .	δ	135EPPARPPPPPAGASPLAEPAAPPSTPAAPKR 166
Db 2460 VQNIİDEKLPFLR 2472	ସ୍ପ	2224 MFGHQKFETVPRPPTPPKDISDEDVKPSTVNLGPSHHHSHPSSPHHSILKHHGDAW 2279
ה היווסמס	λō	167 166
.m. 172515 hvnothetical protein WOAN7 3a - Caenorhabditie elegans	qa	2280 IDFKTVPPCAQNAFSPGBIMFLLAFFVYLSCFASFFSKSLPLLDNLLSLVVYLSISLIIH 2339
information from the process are a constituted and the constitution of the constitutio	- OV	167 166
))	qa	2340 VKHHRKFRWNEEQATTMSKLGAVGRGLYALIAFIVNIVLRVGLNVALVVGVAVSAHBAYK 2399
submitted to the EMBL Data Library, August 1996 A:Reference number: Z20173	ò	167RGSGSSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAXIALALLSVTI 220
A;Accession: T26215 A:Status: preliminary: translated from GB/EMBL/DDBJ	අය	2400 LIKSSGVLRKKBVLDVIYMRDAKKSAIVLSLALLVLFVLAKYPLLTVVTYSLLLALGAAA 2459
A; Wolecule type: DNA A: Residuce 1-7607 / WII.	λο ————————————————————————————————————	221 SFRIYKGVIQAIQKSDEGHPFRAYLESEVAKYSNSALGHVNSTIKELRRLFLV 280
22.2; G	SPDB:GN00023; CESP:Wd Db	2460 GPRVFKKVEAQIKKTDSEHPFSEILAQDLTLPQEKVHAQADVFVEHATCIANKLKKLVFV 2519
A. Layer interior a bource: croise noon. C. Genetics: MACAN 32	· ·	281 DDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKS 340
A; Map position: 5 A:Introns: 1827/1: 1866/3: 1963/3: 1990/3: 2262/1: 2289/1: 2412/1: 2462/2:	2: 2586/2 Db	2520 ESPLESIKFGLVLWSLTYIASWFSGFTLAILGLLGVFSVPKVYBSNQBAIDPHLATISGH 2579
		341 VKDAMAKIQAKIPGLK 356
Query match. Best Local Similarity 13.0%; Prof. No. 3.8e-05; Matches 135; Conservative 78; Mismatches 137; Indels 686; Gaps	B 21;	2580 LKNVQNIIDEKLPPLR 2595
Qy 1 MEDIDQSSLVSSST	14 RESULT	17 6

В. L.,

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A; Molecule type: mRNA
A; Residues: 417-490 <-JE2>
A; Residues: 417-490 <-JE2>
A; Cross-references: GB:M14280; NID:g212607; PIDN:AAA49039.1; PID:g212608
A; Cross-references: GB:M14280; NID:g212607; PIDN:AAA49039.1; PID:g212608
A; Cross-references: GB:M14280; NID:g212607; PIDN:AAA49039.1; PID:g212608
A; Cross-references: GB:M14280; NID:g212607; R.G.; Schrader, W.T.; O'Malley, B.W.
Mol. Endocrinol. 1, 249-259, 1987
A; Reference number: A40911; MUD:88288199; PMID:3453892
A; Reference number: A40911; MUD:88288199; PMID:3453892
A; Residues: 128-133, 'E',135-147,'E',149-164;546-558 <-BIR>
A; Residues: 128-133,'E',135-147,'E',149-164;546-558 <-BIR>
A; Rimpson, R.J.; Grego, B.; Govindan, M.V.; Gronemeyer, H.
Mol. Cell. Endocrinol. 52, 177-184, 1987
A; Title: Peptide sequencing of the chick oriduct progesterone receptor form B.
A; Reference number: A61552; MUD:88005426; PMID:3653503
A; Molecule Vices of the chick original progesterone receptor form B.
A; Molecule Mainer A61552; MUD:88005426; PMID:3653503
                                                                                                                                                                                                                                                                                                                                                residue 21
R.J.; Garni
                                                                                                          R.G.; Maxwell,
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                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 126-133, E', 135-147, E', 149-164 <CO2>
A; Residues: 126-133, E', 135-147, E', 149-164 <CO2>
A; Note: the authors translated the codon CAG for residue 7 as Glu and CAG for R; Joltsch, J.M.; Krozowski, Z.; Quirin-Stricker, C.; Gronemeyer, H.; Simpson, Proc. Natl. Acad. Sci. U.S.A. 83, 5424-5428, 1986
A; Title: Cloning of the chicken progesterone receptor.
A; Reference number: A24312; MUID:86287271; PMID:2426697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 QORBEEEEEEEEDRDCPSYRPGGGSLSKDCLDSVLDTFLAPAAHAAPWSLFGPEVPPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 APMSRGPEQKAVDAGPGAPGPSQP----RPGAPLWPGADSLNVAVKARPGPEDASENRAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 GLPGAEERGFPERDAGPGGGGLAPAAAASPAAV----EPGAGQDYLHVPILPLNSAFLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238 RTRQLLDVEAAYDGSAFGPRSSPSVPAADLAEYGYPPPDGKEGPFAYGEFQSALKIKEEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298 VGLPAAPPPFLGAKAAPADFAQPPRAGQEPSLECVLYKAEPPLLPGAYGPPAAPDSLPST
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A Molecule type: protein

A Residues: 136-153;168-174;195-228;526-537,'X',539;546-563 <SIM>
C;Genetics:
A;Introns: 400/2; 451/1; 490/1; 591/1; 639/2; 683/1; 735/3

A;Introns: 400/2; 451/1; 490/1; 591/1; 639/2; 683/1; 735/3

C;Superfamily: progesterone receptor; erbA transforming protein homology
C;Keywords: DNA binding; nucleus; steroid hormone receptor; zinc finger
F;1-786/Product: progesterone receptor form B #status predicted <AA1>
F;128-786/Product: progesterone receptor form A #status predicted <AA2>
F;491-682/Domain: erbA transforming protein homology <BRBA>
F;491-682/Domain: erbA transforming protein homology <BRBA>
F;421-441/Region: zinc finger
                               A)Residues: 1-64, E, 65-786 < CON>
A)Cross-references: GB:M37518
R)Conneely, O.M.; Sullivan, W.P.; Toft, D.O.; Birnbaumer, M.; Cook, Science 233, 767-770, 1986
A)Title: Molecular cloning of the chicken progesterone receptor.
A)Reference number: A24661; MUID:86289413; PMID:2426779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.9%; Score 272.1; DB 2; Length 7
15.9%; Pred. No. 0.36;
tive 54; Mismatches 119; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121; Conservative
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Best Local S:
Matches 121
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                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-222 <WIL>
A;Cross-references: UNIPROT:Q23188; EMBL:Z78066; PIDN:CAB01523.1; GSPDB:GN00023; CESP:WQ
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A; Residues: 1-786 <GRO>
A; Cross-references: EMBL:Y00092; NID:g63744; PIDN:CAA68282.1; PID:g63745
B; Conneely, O.M.; Dobson, A.D.W.; Tsai, M.J.; Beattie, W.G.; Toft, D.O.; Huckaby, C.S.;
Mol. Endocrinol. 1, 517-525, 1987
A; Title: Sequence and expression of a functional chicken progesterone receptor.
A; Reference number: A40903; MUID:91042592; PMID:3153474
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A;Reference number: S06284; MUID:88166640; PMID:3443098
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R;Gronemeyer, H.; Turcotte, B.; Quirin-Stricker, C.; Bocquel, M.T.; Meyer, M.E.; Krozow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             progesterone receptor form B - chicken
N;Contains: progesterone receptor form A
C;Species: Gallus gallus (chicken)
C;Date:: 18-Nov-1994 #sequence revision 18-Nov-1994 #text change 09-Jul-2004
C;Accession: A35466; S06284; Ā40903; A24661; A24312; A40911; A61552
R;Jeltsch, J.M.; Turcotte, B.; Garnier, J.M.; Lerouge, T.; Krozowski, Z.; Gronemeyer, J. Biol. Chem. 265, 3967-3974, 1990
A;Title: Characterization of multiple mRNAs originating from the chicken progesterone A;Reference number: A35466; MUID:90154085; PMID:2303488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           284 VDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKD 343
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                        Species: Cacnorhabditis elegans
Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 RQPSWERSPAAPAPSLPPAAAVLPSKLPEDDEPPARPPPPPAGASPLAEPAAPPSTPAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164 PKRRGSGSSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFR
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hypothetical protein W06A7.3b - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84;
                                                                                                                                                        submitted to the EMBL Data Library, August 1996
A;Reference number: 220173
A;Accession: T26213
A;Accession: T26213
A;Accession: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.5%; Score 337.5; DB 2
25.7%; Pred. No. 0.0001;
tive 49; Mismatches 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          344 AMAKIQAKIPGLK 356
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Best Local Similarity 25.71
Matches 65; Conservative
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A,Map position: 5
A,Introns: 27/1; 77/2; 201/2
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EMBO J. 6, 3985-3994, 1987
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                                                            C; Date: 15-Oct-1999
C; Accession: T26213
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Thu Jun 23 10:59:55 2005

A; Exper	imental Bource: Btrain 972h-; cosmid c23Al	&	162AAPKR
A; Gene:	A;Gene: SPDB:SPAC23A1.17 A;Gene: Osition: 1	qa	 1258 SPHSNASPSPTSSSMASAAPAR
4 4m./	14 6%. Score 265 5. DB 3.	ò	170 GSSUVDLLYWRDIKKTGVVFGA
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ò	PAAFKYQFVTBPEDEEDEEBEEDEEE	ò	229IQAIQKSDEGHPFRAY)
ପ୍ର	: : : : QDEPSEKDDENKDVEEEQEQEEEQI	qa	1431 NONITQLSQLÓLAPPAQÞSKÁRI
ò	47 DDEDLEELEVLER 59	ď	LVDDLVDSLKFAVLM
qq	: : : : 419 DPEEAKRIALRERMAKMSGGIGMHVFGLPGLAAPIGRKNTLRRTPAKSSEBAKSTTNDSS 478	음	
ò	60KPAAGLS 66	Š	ERHQVQIDHY :
qo	 479 PPKDSSSTSTQPTEQSNAQQAPSPKEBERPLPSEPSQNQPAEYRDTPDTPRNIMPLPGLM 538	අු	1510 KNVGNVTVQQIG
δ	67 AA 68	RESULT	. 10
Ор	: 539 SADQPIKVTEPSNDADKAIVAEGPNNEEETKGPVIPETQETSEQQVHKTPSPEKQKVLSP 598	T13286 Cappuc	cino gene protein - fruit fly
λ	69 4VPPAAAAPLL	C;Spec C;Date	nes: Drosopnia melanogaster :: 13-Aug-1999 #sequence_revisi
ΟP	: : 599 PPIITNFDKETLASNEAHEAVPQKPSAPQVTRLMAPQDSSSVVTPSPTSLLDPARAVRKV 658	C;Acce R;Emmo	ssion: T13286 ns, S.; Phan, H.; Calley, J.;
ò	58 Sd	Genes A,Titl	Dev. 9, 2482-2494, 1995 e: Cappuccino, a Drosophila ma
qq	:	A;Refe A;Acce	rence number: Z17651; MUID:960 ssion: T13286
ò	96 VPPAP 90	A;Stat A;Mole	us: preliminary; translated fr cule type: mRNA
đ	: 719 IDEDKQNEVDPSTSARALPPPGLRFGKVDTLASLAHDDLDDLPAVPRIFSPPPLPKTPSG 778	A;Resi A;Cros	A;Residues: 1-1058 <emm> A;Cross-references: UNIPROT:Q24120;</emm>
ò	91	C;Gene A;Gene	tics: : capu
Op		A;Cros	s-reterences: FlyBase:FBgn0000
'n	94 LPAAPPA 111	Query Ma Best Loc	tch al Similarity 16.2%;
ф		Marc	114
ò	112 111	Š 1	# IDQSSLVS
qq	899 SNVATPPLKQDVTESKASPVADASATHQSSTGLTQEITQLGSNMRLPTKLTRPSNDGRKA 958	<u> </u>	
٥٨	112PAAPAPSLPPAAAV	Ši t	
С	959 SGPRPAAP-PSIPPPLPVSNILSSPTSEPPKDHPPSAPLSKPVSTSPAAPLARVPPVPKL 1017	3	
δ	127 PSK	3 6	NEPANUENTABOUS
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ò	138 137	Ŝ €	
qq	1078 APSGAPPVPAPSGIPPVPKPSVAAPPVPKPSVAVPPVPAPSGAPPVPKPSVAAPPVPVPS 1137	3 , 8	
ò	138 ARPPPPPAGASPLAEP-AAPP	Š €	
QQ	1138 GAPPVPKFSVAAPFVPAPSGAPPVPKPSVAAPPVPAPSSGIPPVPKPAAGVPPVPPPSEA 1197	8 8	
ò	159srp 161	· 음	:
Ор	1198 PPVPKPSVGVPPVPPPSTAPPVPTPSAGLPPVPTAKAPPVPAPSSEAPSVSTPRSSVP 1257	1 8	
4		,	222

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aternal effect rene required for polarity of the egg \epsilon 033799; PMID:7590229
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                                                                                                                                                                                                         :: : | :|:
SVLYMIKEGITGQDKKYKSVHILFPDYSQTVLTATFNPH 1430
                                                                                                                         -SLHRHLSRSSSRASKKPSIVSTTGPFNESFSAKPVEPC 1370
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                                          RISVSRSKSKAERHETSTSSRKSSKSGEHHHHHNEGHAD 1317
                                                                                                                                                                                                                                                                                                  ASLFLLLSLTVF----SIVSVTAYI----- 211
                                                                                                                                                                                                                                                                    YLESEVAISEELVOK----YSNSALGHVNSTIKELRRLF 278
                                                                                                                                                                                                                                                                                                                                                          GAL-----FNGLTLLILALISLFSIPVIY 323
                                                                                                                                                                               TISFRIYKGV---- 228
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-----RGS 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              core 258.5; DB 2; Length 1058;
red. No. 2.1;
Mismatches 103; Indels 435; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen, W;; James, B.; Manseau, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Drosophila melanogaster)
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GEIRPGDIVTFDKAKFSGQK 1540
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Db 746LDFLELLMRFLPTEYERSLITRFEREQRPMEELSEEDRFMLCFSRIPRLPERWTTLT 802 Qy 298 YVGALFNGLTLLIALISL	RESULT 12 RESULT 12 RESULT 12 RESULT 12 RESULT 12 RESULT 12 RESULT 12 RESULT 12 RESULT 12 RESULT 12 RESULT 12 RESULT 12 RESULT 12 RESULT 12 RESULT 13 RESULT 13 RESULT 14 RESULT 15 RESU
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	O.1. NHOBER INNVAREVANJERNANJARANIN NAR HENNESCREDOBLER I VERMATORNIV MI	OY 136 - PPAKPPPPPRAGA	158	Db 994 HBPGPGQLTKSAGPTPEKPEEEATLGDPQLPAETKPPTPAPPKDVTPPKDITPPKDVLPE 1053	Qy 166RR 167	1054 QKTLRPSLSYPLAACDQTRATWPPWHRWGTLPQAAAPLAPIRAPEPLPKGGERRQAAPGR	OY 158	168OSGSSVVDELLYWRDI	: : 1174 PQSCHLGPGAACLSLRGSWEEVGPPSWRNKWHSIRNLPSMRFREQHGEDGVEDMTQLEDL	Oy 183 KKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIY 225 ::	226K	Db 1280 NGRALGENPPHLFAVANLAFAKMLDAKQNQCIIISGESGSGKTEATKLILRYLAAMNQKR 1339	Qy 227 GVIQAIQKSDEGHPFRAYLESEVAISEELVQK 258	1340 EVMQQIKILEATPLLESFGNAKTVRNDNSSRFGKFVEIFLEGGVISGAITSQYLLEKSRI	OY 259 263 DD 1400 VFQAKNERNYHIFYELLAGLPAQLRQAFSLQEAETYYLLNQGGNCEIAGKSDADDFRRLL 1459	Qy 264	Qy 267VNSTIKELRRLFLVDDLVDSLKFAVLM-WVFTYVGAL 302	1520 PEGLQKAITPKVTETMREKIFTPLTVESAVDARDAIAKVLYALLFSWLITRVNALVSP	Qy 303YERHQVQ 329 :	Qy 330 329	Db 1638 ITFADNOPRINLISLKPYGILRILDDQCCFPQATDHTFLQKCHYHHGANPLYSKPKMPLP 1697	330	DD 1698 EFTIKHYAGKVIYQVHKFLDKNHDQVRQDVLDFVKSKIKVVAHLFSSHAFQAAFQKLGK 1/5/	1758 SSSVTRLYKAHTVAAKFQOSLLDLYEKMERCNPLFMRCLKPNHKKEPGL 18	RESULT 14 S11515	formin - mouse C.Species: Mus musculus (house mouse) C.Species: 2-Jan-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004	C. Woychik, R.P.; Maas, R.L.; Zeller, R.; Vogt, T.F.; Leder, P. Nature 346, 850-853, 1990 A,Title: 'Formins': proteins deduced from the alternative transcripts of the limb deformi	
7 26	0 0	309	869	349	914					Jul-2004 .J.; Barber, T.D.; Mi	sin XV genes responsi			:AAF05903.1; PID:g622	Gaps 37;	40	453	45 513	57	573 .	633	65	693	76 753		813 130	873	
229 IOAIOKSDEGHPFRAXIBSEWAISERIVO				RHQVQIDHYLGL	870SVVDLETLAALYENRAQEDELTKIRKYYETSKEEDLKLLDKPEQF	350AKIPGLKRKA 359 :			onventional myosin-15 - human pecies: Homo sapiens (man)	C;Accession. A5926 C;Accession. A5926 R;Liang, Y.; Wang, A.; Belyantseva, I.A.; Anderson, D.W.; Probst, F. an, T.B.; Fridell, R.A.	is 61, 243-258, 1999 is Characterization of the human and mouse unconventional myos	cente number: A59200; Moibizouzi/02; FMID:10352920 1810n: A59200 G. Ataliminatu: Act commared with concentual translation	no. Profiliminary, not compared with conceptual translation. The type: mRNA 1-3530.cLIA>	<pre>1-references: UNIPROT:Q9UKN7; GB:AF144094; NID:g6224682; PIDN: -1887/Domain: myosin motor domain homology <mmo></mmo></pre>	Match 14.1%; Score 256.4; DB 2; Length 3530; Local Similarity 10.1%; Pred. No. 48; les 145; Conservative 54; Mismatches 124; Indels 1106;	17 PPRPPPAFKYQFVTEPEDEEDEEE-	394 PPEVPYFYPEESASAFVYPWVPPPIPSPHNPYAHAMDDIAELEEPEDAGVERQGTSFRLP	41EBDES 1 1 454 SARPEQQGMDKPARSKLSLIRKFRLFPRPQVKLPGKEKLEVPLPPSLDIPLFLGDADEE		514 EDEEELPPVSAVPYGHPFWGFLTPRQRNLQRALSAFGAHRGLGFGPEFGRPVPRPATSLA 58FRKPAAGII	RFLKKTLS		634 RARSSNDARRPPAPQPAPRTLSHWSALLSPPVPPRPPSSGPPPAPPLSPALSGLPRPASP	66SAAAVPPAAAA	PLLDFSSDSVPPAPR	754 AFGFPGASPRASRRRAWSPLASPQPSLRSSPGLGYCSPLAPPSPQLSLRTGPFQP 100 AAAAVLPSKL	814 ÅRRPRSLQESPÅPRRAGRLGPPGSPLPGSPRPSPPLGLCHSPRRSSLNIPSRLPHTWR 131PEDDE	
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            A;Accession: S11515
A;Molecule type: mRNA
A;Residues: 1-1468 <WOY>
A;Cross-references: UNIPROT:Q05860; EMBL:X53599; NID:952877; PIDN:CAA37668.1; PID:952878
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                                                                                                                                                                               602 EEASEKGLGPEKITAPPOHOLPPGIASEGFPCDNFKEQTAKDLPNKDGGVWVPGYRAGPP 661
                                                                                                                                                                                                                                     722 AEYQAAILHLKREHKEEIETLQAQFELKTFHIRGEHALVTARLEEAIENLKQQLEKRREG 781
                                                                                                                                                                                                                                                                                                                                                                      CEEMRDVCISTDDDCSPKAFRNVCIQTDRETFLKPCDAESKATRSSQIVPKKLTISLTQL 841
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C;Species: Caenorhabditis elegans
C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26998
R;Wall, M.
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                                                                                                                         431;
                                                                                          DB 2; Length 1468;
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Reference number: $11515; MUID:90363291; PMID:2392150
                                                                                                                      40; Mismatches 103;
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A;Accession: T26598
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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                                                                                       Score 254.9; D
Pred. No. 6.3;
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Best Local Similarity 14.5%;
Matches 97; Conservative 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168 GSGSSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS----
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                                                                                                                            DB 2; Length 716;
                                                                                                                                                                                                                                                                                                                            EDLEELEV----LERKPAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLP
                                                                                                                                                                             Indels
A;Experimental source: clone Y4886A
Genetics: SESP:
A;Gene: CESP: Y4886A.6
A;Introne: 38/3; 196/3; 437/2; 460/3; 518/1; 617/3; 673/3
                                                                                                                                                                           39; Mismatches 106;
                                                                                                                            14.0%; Score 254.7; 16.9%; Pred. No. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             completed: June 23, 2005, 10:56:54
le : 32.9653 secs
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                                                                                                                                                   Best Local Siminary
Matches 101; Conservative
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                                                                                                                            Query Match
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GenCore version 5.1.6
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OM protein - protein search, using sw model Run on:

June 23, 2005, 10:17:56 ; Search time 113.842 Seconds (without alignments) 1619.338 Million cell updates/sec

1823 1 MEDIDQSSLVSSSTDSPPRP.....VKDAMAKIQAKIPGLKRKAD 360 US-09-830-972-2-FUSED Perfect score:

Gapop 10.0 , Gapext 0.1 **BLOSUM62** Scoring table:

Sequence:

1612378 seqs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

uniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Pred. No.

SUMMARIES

Description	09ikll rattus norv	Q8bh78 mus musculu	mus	Q8k3g7 mus musculu	Q8bgm9 mus musculu	Q8k3g8 mus musculu	homo	homo	Q6ipn0 homo sapien	homo	แนย	Q80w95 mus musculu	Q8k290 mus musculu	Q6rss8 gallus gall	_	pog	Q6im70 sus scrofa	Q6ify4 xenopus tro	sus scr	Q7pcj7 macaca fasc	Q6jrv2 xenopus lae	Q6jrv0 xenopus lae	Q6jrv7 xenopus lae	Q6jrv1 xenopus lae	Q6jrv4 xenopus lae	xenobne	Q6jrv3 xenopus lae	xenopu	gallus g	xenopu	Q6jrwl xenopus lae
ID	RTN4 RAT	Q8BH <u>7</u> 8	QBBHF5	Q8K3G7	Q8BGM9	Q8K3G8	Q96B16	RTN4_HUMAN	QGIPNO	Q8IUA4	Q8BGK7	Q80W95	Q8K290	Q6RSSB	RTN4 MOUSE	Q7YRW9	Q61M70	Q6IFY4	Q61G15	Q7PCJ7	Q6JRV2	Q6JRV0	Q6JRV7	Q6JRV1	Q6JRV4	QGJRVB	Q6JRV3	Q6JRV9	Q7T224	QGJRWO	Q6JRW1
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Length	1163	356	375	357	1162	1163	392	1192	343	986	1046	578	639	658	199	199	199	315	187	199	1024	1043	1032	1055	330	1044	311	1013	199	304	323
* Query Match	95.0	94.4	93.9	93.9	89.8	89.0	87.7	83.3	80.7	55.5	55.4	54.4	54.2	52.7	50.1	49.6	49.4	49.3	49.1	49.1	48.6	•	48.5	48.5	48.4	48.3	48.3	48.2	48.0	47.7	47.7
	1732.7	1721.6	1712.7	1711.5	1637	1622.9	1598.4	1518.4	1471.5	1012.1	1010.2	992.2	988.7	960.5	914	904	o	899.1	968	895	886.4	884.5	٠	883.3		٠	880.5	878.7	874.8	870.4	870.3
Result No.		8	m	4	S	9	7	89	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29.	30	31

similarity).
SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the membrane of the endoplasmic reticulum through 2 putative transmembrane domains (By similarity).

Event-Alternative splicing; Named isoforms=4; Name=1; Synonyms=Nogo-A, NI-220-250;

ALTERNATIVE PRODUCTS

-

similarity). -1- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2

	Q6jrw4 xenopus lae Q7t222 carassius a
QGURW2 Q7TNB7 QQGN33 RTN1 HUMAN QBKOTO QBKS4 RTN1 RAT Q90638 QGFP23 QGFP23 QGFP23	Q6JRW4 Q7T222
0000000000000000	0 0
316 720 776 776 777 777 760 193	214
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	40.8 40.4
961.2 855.6 826.3 826.3 823.2 823.2 807.4 793.9 766.1	744 736.6
и и и и и и и и и и и и и и и и и и и	4 4 5 4

ALIGNMENTS

RESULT 1

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SEQUENCE FROM N.A. (ISOFORM 3), AND PARTIAL SEQUENCE.
STRAIN=Spreague-Dawley, TISSUE=Addipocyte;
MEDLINE=9249816; PubMed=10231557; DOI=10.1016/S0167-4889(99)00033-6;
MOTTIS N.J., ROSS S.A., Neveu J.M., Lane W.S., Lienhard G.E.;
"Cloning and characterization of a 22 kDa protein from rat adipocytes: a new member of the reticulon family.";
Biochim. Biophys. Acta 1450:68-76(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: Potent neurite outgrowth inhibitor which may also help block the regeneration of the nervous central system in adults (By
                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORMS 2 AND 4).
STRAIN-WHIGHER KYDOO, TISSUE-VASCUlar smooth muscle;
Ito T., Schwartz S.M.;
"Cloning of a member of the reticulon gene family in rat: one of two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GrandPre T., Li S., Strittmatter S.M.;
"Nogo-66 receptor antagonist peptide promotes axonal regeneration.";
Nature 417:547-551(2002).
                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20129258; PubMed=10667796; DOI=10.1038/35000219; MEDLINE=20129258; PubMed=10667796; DOI=10.1038/35000219; Dilnann A.S., Huber A.B., Van der Haar M.E., Frank M., Schnell L., Spillmann A.A., Christ F., Schwab M.E.; Frank M., Schnell L., "Nogo-A is a myelin-associated neurite outgrowth inhibitor and antigen for monoclonal antibody IN-1."; Mature 403:434-439(2000).
            Q9JKII; Q9JKIO; Q9RODS; Q9WUE9; Q9WUF0; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 65-UUL-2004 (Rel. 44, Last annotation update) Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  minor splice variants.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22033691; PubMed=12037567; DOI=10.1038/417547a;
1163 AA
                                                                                                             (Glut4 vesicle 20 kDa protein).
                                                                                                                                    Name=Rtn4; Synonyms=Nogo;
STANDARD;
                                                                                                                                                        Rattus norvegicus (Rat)
                                                                                                                                                                                                           NCBI_TaxID=10116;
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N

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1020
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                                                                                                                     181 AASEPVIPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYL 240
                                                                                                                                                                                                                                                                              301 AILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDIFNEMQMSVVA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          541 NEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSL 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      841 IIDBFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK 900
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                                                                                                                                                                                                241 GNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSSFKGSPKGES
                                                                                                                                                                                                                                                                                                                                                                                                                                    421 NEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTSENKTDEKKIEERKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 481 QIITEKTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     601 LPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 901 DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKED
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                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
          Name=2; Synonyms=Nogo-B, Foocen-M1; Isold=09JKI1-2; Sequence=VSP_005658; Name=3; Synonyms=Nogo-C, VP20; Isold=09JKI1-2; Sequence=VSP_005656, VSP_005657; Name=4; Synonyms=Poocen-M2; Isold=09JKI1-4; Sequence=VSP_005659; are present in optic nerve, spinal cord and cerebral cortex. Isoforms 1 and 2 are present in dorsal root ganglion, sciatic nerve and PC12 cells after Longer exposure. Isoforms 2 and 3 are detected in kidney, cartilage, skin, lung and spleen. Isoform 3 is expressed at high level in skeletal muscle. In adult animals isoform 1 is expressed mainly in the nervous system.
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EMBL; AJ242961; CAB71027.1; -.
EMBL; AJ242962; CAB71028.1; -.
EMBL; AJ242962; CAB71029.1; -.
EMBL; AJ32045; AAD31019.1; -.
EMBL; AF132046; AAD31009.1; -.
EMBL; AF132046; AAD31009.1; -.
EMBL; AF132046; Clintegral to endoplasmic reticulum membrane; IDA.
GO; GO:000515; Clintegral to endoplasmic reticulum membrane; IDA.
GO; GO:000515; F:protein binding; ISS.
GO; GO:0019987; P:negative regulation of anti-apoptosis; ISS.
GO; GO:0030517; P:negative regulation of axon extension; ISS.
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/FIId=VSP 005658.
Missing (in isoform 4).
FTIG=VSP 005659.
Missing (in Ref. 3; AAD31020).
MW; 8CB894B09E94F0B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytoplasmic (Potential). Reticulon.
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Potential.
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Alternative splicing; Direct protein sequencing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lumenal (Potential)
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Pred. No. 1.2e-47;
0; Mismatches 0;
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IsoId=Q9JK11-1; Sequence=Displayed;
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31.0%;
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1163 AA; 126386
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PROSITE; PS5084
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                                                                                                                                                                                                                                                                                                                       STRAIN=129/SvcJ7, and 129SvcJ7;
MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
Oertle T., Huber C., van der Putten H., Schwab M.E.;
"Genomic structure and functional characterisation of the promoters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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Pred. No. 1.6e-48;
2; Mismatches 7; Indels
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EMBL; AY102281; AAM73503.1; -.
EMBL; AY102286; AAM73508.1; -.
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Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                             Last sequence update)
Last annotation update)
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GO; GO:0005783; C:endoplasmic reticulum; IDA.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0001225; F:angiogenesis; IMP.
GO; GO:0007399; P:neurogenesis; IDA.
                                              356 AA
                                                                                         Created)
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J. Mol. Biol. 325:299-323(2003).
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Van der Putten H., Mir A.;
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                                                 PRELIMINARY;
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                                                                                                                                                                           Name=Rtn4;
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119 PAAAVLPSKLPEDDEPPAR--PPAPAGASPLAEPAAPPSTPAAPKRKGSGSVDETLFALP 176
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                                                                                                                                                                                                                                                                                                                                 STRAIN=129/SvcJ7, and 129SvcJ7;
MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
OGertle T., Huber C., van druder Putten H., Schwab M.E.;
"Genomic structure and functional characterisation of the promoters of
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Best Local Similarity 91.6%; Pred. No. 3.6e-48;
Matches 347; Conservative 3; Mismatches 6; Indels 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=1298vcJ7;
Van der Putten H., Mir A.;
Submitted (Mar.2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AX102282; AAM73504.1; -.
EMBL; AX102286; AAM73509.1; -.
GO; GO:0005783; C:endoplasmic reticulum; IDA.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0005515; P:protein binding; IPI.
GO; GO:0001359; P:proteins binding; IMP.
GO; GO:0007399; P:neurogenesis; IMP.
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Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases
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PROSITE; PS50845; RETICULON; 1.
SROUENCE 375 AA; 40300 MW; 23D9EB19BE671AE6 CRC64;
                                                                           Last sequence update)
Last annotation update)
375 AA
                                                  Created)
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J. Mol. Biol. 325:299-323(2003)
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297 AMLVENTKEEVIVRSKDKEDLVCSAALHNPQESPATLTKVVKEDGVMSPEKTMDIFNEMK 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177 AASEPVIPSSAEKIMDLKEQPGNTVSSGQEDFPSVLPETAASLPSLSPLSTVSFKEHGYL 236
                                                                STRAIN=129/SvcJ7, and 129SvcJ7, which is a state of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the promoters of the p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Indels 810;
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Pfam; PP02453; Reticulon; 1.
PR051TE; PS50945; RETICULON; 1.
SEQUENCE 1162 AA; 126612 MW; 855697FBEE11781F CRC64;
                                                                                                                                                                                                                                                                                                                                                     STRAIN=129SvcJ7;
Van der Putten H., Mir A.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AX102284; ARM73506.1; -.
EMBL; AX102286; ARM73511.1; -.
MGD; MGI:1915835; Rtn4.
                                                                                                                                                                                                                                                                                       to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDA
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GO; GO:0005515; F:protein binding; IPI.
GO; GO:0001525; P:angiogenesis; IMP.
GO; GO:0007399; P:neurogenesis; IDA.
                                                                                                                                                         human and mouse nogo/rtn4.";
J. Mol. Biol. 325:299-323(2003)
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                                                                                                                                                                                                                                                                                       Submitted (MAY-2002)
                                                                                                                                                                                                                                                                  Van der Putten H.;
                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                STRAIN=129/SvcJ7;
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIKKTGVVYFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGH
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                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name-Rtn4;
Nus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93.9%; Score 1711.5; DB 2; Length
96.1%; Pred. No. 3.5e-48;
ive 2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                         Jin W., Li R., Long M., Shen J., Ju G.;
Submitted (MAX-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AX114153; AAM77069.1; -.
MGD; MGI:1915835; Rtn4.
GO; GO:0005783; C:endoplasmic reticulum; IEA.
InterPro; IPR03389; Reticulon.
PROSITE: PSS0845; RETICULON; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            357 AA; 38566 MW; 73BB3D17DFDBDF15 CRC64;
                                                                                                                                                    Last sequence update)
Last annotation update)
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                                                                                                                             (TrEMBLrel. 22, (TrEMBLrel. 22, 1 (TrEMBLrel. 26, 1
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23,
27,
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                                                                                    PRELIMINARY;
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STRAIN=BALB/c;
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01-OCT-2002 (
01-MAR-2004 (
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01-MAR-2003
05-JUL-2004
                                                                                                                                                                                                                       Name=Rtn4;
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08BGM9
1D 08BG
AC 08BG
DT 01-M
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118

59

171

qq	537 CESELNEATGTKIAYETKVDLVQTSEAIQESIYPTAQLCPSFEEAEATPSPVLPDIVMEA 596	ò	1 MEDIDOSSIVSSTDSPPRPPPAFKYOFVTEPEDEEDEEEEDBEEDBEDLEELEVLERK 60
ò	172 171	q	
ф	597 PINSLIPSTGASVAQPSASPLEVPSPVSYDGIKLEPENPPPYEEAMSVALKTSDSKEEIK 656	È	61 PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPBRQPSWERSPAAPABSLP 120
È	172 171	qq	60 PAAGLSAVPVPP-AAAPLLDFSSDSVPPAPRGPLPAAPPTAPERQPSWERSPAASAPSLP 118
qq	657 EPESFNAAAQEAEAPYISIACDLIKETKLSTEPSPEFSNYSEIAKFEKSVPDHCELVDDS 716	ò	121 PAAAVLPSKLPEDDEPPARPPPPPAGASPLAEPAAPPSTPAAPKRRGSGS 1,71
ò	172 171	qq	119 PAAAVLPSKLPEDDEPPARPPAPAGASPLAEPAAPPSTPAAPKRGSGSVDETLFALP 176
qa	717 SPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVSETVTQHKHKERLSASPQEVGKPY 776	ò	172 171
à	172 171	QQ	177 AASEPVIPSSAEKIMDLKEQPGNTVSSGQEDPPSVLFETAASLPSLSPLSTVSFKEHGYL 236
qq	777 LESFOPNLHITKDAASNEIPTLTKKETISLOMEEFNTAIYSNDDLLSSKEDKMKESETFS 836	ò	172 171
à	172 171	q	237 GNLSAVASTEGTIEETLANEASRELPERATNPFVARESAEFSVLEYSEMGSSFNGSPKGES 296
Ωp	837 DSSPIEIIDEFPTFVSAKDDSPKEYTDLEVSNKSEIANVQSGANSLPCSELPCDLSFKNT 896	ò	172 171
λ	172 171	qq	297 AMLVENTKEEVIVRSKDKEDLVCSAALHNPQESPATLTKVVKEDGVMSPEKTMDIFNEMK 356
Ор	897 YPKDEAHVSDEFSKSRSSVSKVPLLLPNVSALESQIEMGNIVKPKVLTKEAEEKLPSDTE 956	ò	172 171
ò	172SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAXIALA 214	qu	357 MSVVAPVREEYADFKPFEQAWEVKDTYEGSRDVLAARANMESKVDKKCFEDSLEQKSHGK 416
DP	957 KEDRSLTAVLSAELNKTSVVDLLYMRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALA 1016	ò	172 171
ò	215 LLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAKYSNSALGHVNSTIKEL 274	qa	417 DSESRNENASFPSTPELVKDGSRAYITCDSFTSATESTAANIFPVLEDHTSENKTDEKKI 476
QQ Q	1017 LLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKEL 1076	ζ	172 171
ò	275 RRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYL 334	q	477 EERKAQIITEKTSPKTSNPFLVAIHDSEADYVTTDNLSKVTEAVVATMPEGLTPDLVQEA 536
Ор	1077 RRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIFVIYERHQAQIDHYL 1136	ò	172 171
ò	335 GLANKSVKDAMAKIQAKIPGLKRKAD 360	qq	537 CESELNEATGTKIAYETKVDLVQTSEAIQESIYPTAQLCPSFEEAEATPSPVLPDIVMEA 596
Dp	1137 GLANKSVKDAMAKIQAKIPGLKRKAE 1162	ò	172 171
		qq	597 PLNSLLPSTGASVAQPSASPLEVPSPVSYDGIKLEPENPPPYEEAMSVALKTSDAKEEIK 656
200		ò	172 171
	PRELIMINARY;	QQ	657 EPESFNAAAQEAEAPYISIACDLIKETKLSTEPSPGFSNYSEIAKFEKSVPDHCELVDDS 716
	01-001-2002 (Trimbrel. 22, Created) 01-007-2002 (Trimbrel. 22, Last sequence update)	ò	172 171
	(Tremburel. 26,	qq	717 SPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVSETVTQHKHKERLSASPQEVGKPY 776
	Name=KC114; Mus musculus (Mouse).	ò	172 171
	bukaiyota; metazoa; chotaata; craniata; vertebrata; butercostoni; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Moor maarin-indoo.	Dp	777 LESFQPNLHITKDAASNEIPTLTKKETISLQMEEFNTAIYSNDDLLSSKEDKMKESETFS 836
		à	172 171
	SEQUENCE FROM N.A. STRAIN-BALB/C;	q	837 DSSPIEIIDEFPTFVSAKDDSPKEYTDLEVSNKSEIANVQSGANSLPCSELPCDLSFKNT 896
	mitted (MAY-2002) to the BMBL/GenBank/DDBJ databases.	ò	172 171
	1); MGI:1915835; RAM //068.1;	q	897 YPKDEAHVSDEFSKSRSSVSKVPLLLPNVSALESQIEMGNIVKPKVLTKEAEEKLPSDTE 956
DR GO;	GO; GO:0005/83; C:encoplammic reciculum; 1kA. Interpro; IPR003388; Reticulon. Pf=m: DF07453: Det(culon. 1	, &	172SVVDLLYMRDIKKTGVV-FGASLFLLLSLTVPSIVSVTAXIAL 213
	FIGHT, FF0233, NCLICATION, 1. PROSITE, PS50845, RETICULOM, 1. PROSITENCE 1163 AA: 126690 MW: 6RSF362799417EA4 CRC64:	q	957 KEDRSLTAVLSAELNKTSVVDLLYWRDIKKTGVVYFGASLFLLLSLTVFSIVSVTAYIAL 1016
Ouerv	3 Score 1622.9: DB 2:	ò	214 ALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKE 273
Best L	Indela	qq	1017 ALLSVIISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKE 1076
		ò	274 LRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHY 333

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115

9 58 166

238

298

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PAAGLSAAAVP--PAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       239 VTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGH
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                                MEDIDQSSLVSSSTDSPPRPPARKYQFVTEPEDEEDEEBEEDEEEDBEDLEBLEVLERK
                                                                                                                                                                                                                                              116 APSLPPAAAVLPSKLPEDDEPPARPPPPPAGASPLAE------PAAPPSTPAAPKR
                                                                                                                                                                                                                                                                                                                                                      -----GSSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVS
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Jin W.-L., Ju G.;
Povelopmentally-regulated alternative splicing in a novel Nogo-A.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
MEDLINE=20129242; PubMed=10667780; DOI=10.1038/35000287;
Prinjha R., Moore S.E., Vinnon M., Blake S., Morrow R., Christie G., Michalovich D., Simmons D.L., Walsh F.S.;
"Inhibitor of neurice outgrowth in humans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-21010696; PubMed-11126360; DOI=10.1038/sj.onc.1203948; Tagami S., Eguchi Y., Kinoshita M., Takeda M., Tsujimoto Y.; Ah novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 on endoplasmic reticulum and reduces their anti-apoptotic activity."; Oncogene 19:5736-5746(2000).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)
(Neurcendocrine-specific protein) (NSP) (Neurcendocrine specific protein C homolog) (RTN-x) (Reticulon 5) (My043 protein).
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Q9NQC3; Q94962; Q9BXG5; Q9H212; Q9H313; Q9UQ42; Q9Y293; Q9Y2Y7;
Q9Y5U6;
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"Assignment of the human reticulon 4 gene (RTN4) to chromosome 2p14-->2p13 by radiation hybrid mapping.";
Cytogenet. Cell Genet. 88:101-102(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       327 QVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 360
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MEDLINE=20237542; PubMed=10773680;
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Nature 403:383-384(2000)
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RIN4 HUMAN
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A Itzaubberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,

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T. "Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
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PROSITE; PS50845; RETICULON; 1.
SEQUENCE 392 AA; 42274 MW; D7B2AA5E839E58AD CRC64;
                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Reticulon 4, isoform D (RTW4 isoform B2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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GO; GO:0005783; C:endoplasmic reticulum; IEA.
InterPro; IPR003388; Reticulon.
                                                                                                                                                                                                                                                                    392 AA
                                                                                                                LGLANKSVKDAMAKIQAKIPGLKRKAD 360
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J. Mol. Biol. 325:299-323(2003)
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Matches 326; Conservative
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                                                                               334
                                                                                                                                1137
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REQUENCE FROM N.A. (ISOFORMS 2 AND 3).

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REDINELS-238825; PubMed=12477932; DOI=10.1073/ppas 242603899;

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R. Generation and initial analysis of more than 15,000 full-length human
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MBDLNRE-20499367; PubMed=11042152; DOI=10.1101/gr.140200;
Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,
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"Cloning and functional analysis of cDNAs with open reading frames for atem/progenitor cells.";
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Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
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The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro.";
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Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
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                                                                                                                                                                                                       Yutsudo M.;
"Isolation of a cell death-inducing gene.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                           TISSUE=Placenta, and Skeletal muscle;
Ito T., Schwartz S.M.;
"Cloning of a member of the reticulon
[5]
SEQUENCE FROM N.A. (ISOFORMS 2 AND 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 3).
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                                                                                                                                                                                 TISSUE=Fibroblast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yu J., Han L.H.; "Novel human cDN?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rissuE=Brain;
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ISOSUB SPECIFICITY: Isoform 1 is specifically expressed in brain
and testis and weakly in heart and skeletal muscle. Isoform 2 is
widely expressed excepted for the liver. Isoform 3 is expressed in
brain, skeletal muscle and adipocytes. Isoform 4 is testis-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Neurosci. Res. 67:559-565 (2002).

J. Neurosci. Res. 67:559-565 (2002).

J. Neurosci. Res. 67:559-565 (2002).

J. Neurosci. Res. 67:559-565 (2002).

J. Schort in the regeneration of the nervous central system in adults. Block the regeneration of the nervous central system in adults. Instituted in reduction of the neuroscitic activity of Bcl-1 and Bcl-2. This is likely consecutive to their change in subcellular location, from the micochondria to the endoplasmic reticulum, after binding and sequestration.

J. SUBUNIT: Binds to RTNR. Interacts with Bcl-xl and Bcl-2.

J. SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic reticulum through 2 putative transmembrane of the endoplasmic reticulum through 2 putative transmembrane domains.
                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21069055; PubMed=11201742; DOI=10.1038/35053072;
Fournier A.E., Grandpre T., Strittmatter S.M.;
"Identification of a receptor mediating Nogo-66 inhibition of axonal
                                                                                                                                                                                                                                                                       GrandPre T., Nakamura F., Vartanian T., Strittmatter S.M.; "Identification of the Nogo inhibitor of axon regeneration as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21888956; PubMed=11891768; DOI=10.1002/jnr.10134; Ng C.E.L., Tang B.L.; "Nogos and the Nogo-66 receptor: factors inhibiting CNS neuron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEMILARITY: Contains 1 reticulon domain. CAUTION: Ref.11 sequence differs from that shown due to frameshifts in positions 1149 and 1156.
                                                                                                                                                                                                                                                      MEDLINE=20129259; PubMed=10667797; DOI=10.1038/35000226;
                                       Mao Y.M., Xie Y., Zheng Z.H.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                             Sha J.H., Zhou Z.M., Li J.M.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Event-Alternative splicing; Named isoforms=4;
Mame=1; Synonyms=RTN 4A, NOGO-A, RTN-XL;
Isold=QNNC3-1; Sequence=Displayed;
Name=2; Synonyms=RTN 4B, NOGO-B, RTN-XS, Foocen-M;
Isold=QNNC3-2; Sequence=VSP 005555;
Name=3; Synonyms=RTN 4C, NOGO-C, Foocen-S;
Isold=Q9NQC3-3; Sequence=VSP_005552, VSP_00553;
SEQUENCE OF 482-1192 FROM N.A. (ISOFORM 1/4)
                                                                                                     SEQUENCE OF 186-1192 FROM N.A. (ISOFORM 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AJ251384; CAB99249.1; -. AJ251385; CAB99250.1; -. AB040462; BAB18927.1; -.
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                                                                                                                                                                                                                                                                                                                                        Nature 403:439-444(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 409:341-346(2001)
                                                                                                                                                                                                                                                                                                                 Reticulon protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            regeneration.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          regeneration.";
                                                                                                                              (SSUE=Testis;
                                                                                                                                                                                                                               TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION.
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Klausner R.D., Colling F.S., Wagner L.H., Derge J.G.,
Altausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A popking R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brownstein M.J., Usdin T.B., Tochhiyuki S., Carninci P., Frange C.,
Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., García A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., García A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Krzywinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,
A. Jones S.J., Marra M.A.,
T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                      1079 SEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMMVFTYVGALFNGL 1138
                                                                                                                                                                               959 ATQABIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTG 1018
                                                                                                                                                                                                                     246
                                  839 VYSNDDLFISKEAQIRETETFSDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKS
                                                                                                        899 EIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSAL
                                                                                                                                                                                                                   WYEGASLFLLISLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLE
                                                                                                                                                                                                                                                                                             SEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGL
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases EMBL, BC071848; AAH71848.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
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GO, GO:0005783; C:endoplasmic reticulum; IEA.
Intervo, IPR003388; Reticulon.
Pfam, PF02453; Reticulon; 1.
PROSITE; PS50845; RETICULON; 1.
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                                                                                                                                                                                                                                    DB 1; Length 1192;
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                                                                                                                                                                                                                                    83.3%; Score 1518.4; 27.3%; Pred. No. 1.3e
                                                                                                                                                                                                                                                                      12; Mismatches
                                                                                                                                                          BAA74909.2; ALT_INIT. AAH01035.1; -.
                                                                                                                      AAD27783.1;
AAG17976.1;
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AAD31022.1;
                                                   AAG40878.1;
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               AAG12177.1;
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                                                                                                                                                                                                                                                                        326; Conservative
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AF148537
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                                                                                                                                                                                                                         GPLPAAPPAAPEROPSWERSPAA---PAPSLPPAAAVLPSKLPEDDEPPARPPPPAGA 148
                                                                                                                                                                                                                                                   62 GPLPAAPPVAPERQPSWDPSPVSSTVPAPSPLSAAAVSPSKLPEDDEPPARPPPPPASV 121
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
NY4 (RTN4 isoform Ab) (RTN4 isoform D) (RTN4 isoform B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oertle T., Huber C., van der Putten H., Schwab M.E.; Genomic structure and functional characterisation of the promoters of human and mouse nogo/rtn4.".
J. Mol. Biol. 325:299-323(2003).
                                                                                                                                                        122 SPQAEPVWTPPAPAPAAPPSTPAAPKRRGSSGSVVVDLLYWRDIKKTGVVFGASLFLLLS
                                                                                                                                                                                                                                                                                                                                                                                                                            SPLAE-----PAAPPSTPAAPKRRG-SGSSVVDLLYWRDIKKTGVVFGASLFLLLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFS
                                                                                                                                 34 DEEDEEEEEEEEEEDEEDLEELEVLERKPAAGLSAAAVP--PAAAAPLLDFSSDSVPPAPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                        15;
                                              DB 2; Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-TEACH (MAY-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY102285; AAM64244.1; -.
EMBL; AY123246; AAM64250.1; -.
EMBL; AY123249; AAM64251.1; -.
EMBL; AY123249; AAM64253.1; -.
EMBL; AY123250; AAM64254.1; -.
EMBL; AY123345; AAM64254.1; -.
EMBL; AY123345; AAM64254.1; -.
EMBL; AY123345; AAM64254.1; -.
EMBL; AY123345; AAM64254.1; -.
EMBL; AY123345; AAM64254.1; -.
EMBL; AY123345; AAM64254.1; -.
EMBL; AY123345; AAM64254.1; -.
EMBL; AY123345; AAM64254.1; -.
EMBL; AY123345; AAM64254.1; -.
                                                                                     17; Indels
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813207C29AB15BA4 CRC64;
                                       80.7%; Score 1471.5; DB 3
86.8%; Pred. No. 2.3e-40;
ive 13; Mismatches 17;
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Submitted (MAY-2002) to the EMBL/GenBank/DDBJ
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36918 MW;
                                     Query Match
Best Local Similarity 86.84
Matches 297; Conservative
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343
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SEQUENCE
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081UAA
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                                                                                                                                                                                                                                                                                                                                                                           -----EVLERKPAAGLSAAVPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----AAPLLDFSSDS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    264 AATESIATNIFPLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          324 VITDNLTKVTEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    384 LYPAAQLCPSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESI
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                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----VPPAPRGPLPAAPPAAPERQ-------VPPAPRGPLPAAPERQ-------
                                                                                                         549;
                                                 55.5%; Score 1012.1; DB 2; Length 986; 27.7%; Pred. No. 3.3e-24; ive 33; Mismatches 71; Indels 549;
OCDE8F647036415A CRC64;
                                                                                                                                                           DIDQSSLVSSSTDSPPRPPAFKYQFVTRPEDE----EDEEE---
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Matches 250; Conservative
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975 FAVLMMVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKI 1034
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                                                                                                                                                                                                                                                                     795 SRSSVSKVPLLLPNVSALESQIEMGNIVKPKVLTKEAEEKLPSDTEKEDRSLTAVLSAEL 854
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  615 IPEVPOTOEEAVMLMKESLTEVSETVTOHKHKERLSASPOEVGKPYLESPOPNLHITKDA
                                                                                                                  675 ASNEIPTLTKKETISLQMEEFNTAIYSNDDLLSSKEDKMKESETFSDSSPIEIIDEFPTF
                                                                                                                                                                                          735 VSAKDDSPKEYTDLEVSNKSEIANVQSGANSLPCSELPCDLSFKNTYPKDEAHVSDEFSK
                                                                                                                                                                                                                                171
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                                                                                                                                                                                                                                                                                                          171 --SSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 GLS-----AAAVP----PAAAAPLLDFSSDSVPPAPR-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tozaki H., Hirata T.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB073672; BAC75974.1; -.
GO; GO:0005783; C:endoplasmic reticulum; IEA.
InterPro; IFR003388; Reticulon.
Pfam; PF02453; Reticulon; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      578 AA; 63696 MW; 832670C171E4AC61 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54.4%; Score 992.2; DB 2; 42.4%; Pred. No. 4.1e-24; ive 13; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 PPRPPP---AFKYQFVTEPEDEEDEEBDEEDDE---
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   157 PPSTP
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                                                                                                                                                                                                                                           STRAIN=129/SvcJ7, and 1298vcJ7;
MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
Oertle T., Huber C., van der Putten H., Schwab M.E.;
"Genomic structure and functional characterisation of the promoters of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       257 FEQAWEVKDTYEGSRDVLAARANMESKVDKKCFEDSLEQKGHGKDSESRNENASFPRTPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----PSWERSPAAPAPSLP----PAAAVLPSKLPEDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DKEDLVCSAALHNPQESPATLTKVVKEDGVMSPEKTMDIFNEMKMSVVAPVREEYADFKP
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                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55.4%; Score 1010.2; DB 2; Length 1046; 29.2%; Pred. No. 4.3e-24; ive 25; Mismatches 80; Indels 498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ·-----EDEBEEDEEEDED
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Van der Putten H.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
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Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY102286; AAM73502.1; --
EMBL; AY102286; AAM73507.1; --
                                                         Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:1915835; Rtn4.
GO; GO:0005783; C:endoplasmic reticulum; IDA.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0001252; F:angiogenesis; IMP.
GO; GO:0007399; P:neurogenesis; IDA.
InterPro; IPRO$03388; Reticulon.
PRO$1TE; P$$50845; RETICULON; 1.
 1046 AA
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                                     Created)
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J. Mol. Biol. 325:299-323(2003).
                                   23,
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Matches 249; Conservative
PRELIMINARY;
                                   01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
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                                                                                                                               Mus musculus (Mouse).
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                                                                                                                                                                                          NCBI_TaxID=10090;
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                                                                                                              Name=Rtn4;
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                                                                                                                                            -- SWERSPAAPAPSLPPAAAVLPS-
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  VSETVTQHKHKERLSASPQEVGKPYLESFQPNLHITKDAASNEIPTLTKKETISLQMEEF
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
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01-OCT-2002 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
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Name=Rtn4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         -----SWERSPAAPASLPPAAVLPS-
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caltharp S.A., Pira C.U., McNeill D.S., Liwnicz B.H., Oberg K.C.; Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AX494005; AAS18427.1; -.
GO; GO:0005783; C:endoplasmic reticulum; IEA.
                                                                                                                                                         Indels 225;
                                                                                                                                                                                                                                                  64 GLS-----AAAVP-----PAAAPLLDFSSDSVPPAPR-----
                                                                                                                          Length 639;
                                                                                            70312 MW; 309A19DA37603F11 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                          DB 2;
                                                                                                                         54.2%; Score 988.7; DB 2 42.2%; Pred. No. 6.8e-24;
                                                                                                                                                                                      PPRPPP---AFKYQFVTEPEDEEDEEEEDEEDDE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence upd
05-JUL-2004 (TrEMBLrel. 27, Last annotation u)
Neurite outgrowth inhibitor NOGO-A (Fragment)
EMBL; BC032192; AAH32192.1; -. MGD; MGI:191885; Rtn4.
GQD; MGI:191885; Rtn4.
GQD; GO:0005783; C:endoplasmic reticulum; IEA
InterPro; IPR003388; Reticulon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  658 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   409 IEMGNIVKPKVLTKEAEEKLPSDTEKEDR----
                                                                                                                                                       14; Mismatches
                                                                                                                                                                                                                                                                                                               -----GPLPAAPPAAPERQP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                          Pfam; PF02453; Reticulon; 1.
PROSITE; PS50845; RETICULON; 1.
SEQUENCE 639 AA; 70312 MW;
                                                                                                                                                       Matches 232; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       351 KIPGLKRKAD 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus gallus (Chicken)
                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=NOGO
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Best Local
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Q6RSS8
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Gaps 16;
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                                                                                                                                                                                                                                                                                                     152 PYISIACDLIKETKVSGESASPSLTDYSTTPITEHLSQDVSEHKELAEKLSPQFGKCDLF 211
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                                                                                                                                                                                DLVQTSESVQETLKPVTQLCPSPEDSEAAPSPVLPDIVMEAPLSSGTAGAEASTVQLETS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       494 ILSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESDVAVSEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                      Indels 305;
                                                                                        ; Score 960.5; DB 2; Length 658;
; Pred. No. 6.1e-23;
41; Mismatches 70; Indels 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           614 LFSVPVIYERHQAQIDHYLGLVNKNVKDAMAKIQAKIPGLKRKTE 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RTM4 MOUSE STANDARD; PRT; 199 AA.
295P72; OGCTE3;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2004 (Rel. 44, Last annotation update)
Reliculon 4 (Neurite ougrowth inhibitor) (Nogo protein).
Name=Rtn4; Synonyms=NOGO;
Mus musculus (Mouse).
                                                           72075 MW; 14B7A000C5E8CDA5 CRC64;
                                                                                                                                                    DIDQSS----LVSSSTDSPPRPPAF---
                                                                                                                                                                                                                                                                                                                                 35 -----EEDEEE------EEDEEED-
                                                                                                                                                                                                               ------KYOFV-----
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STRALM-317-L.I. TISSUE=Adipocyte;
Coulson A.C., Craggs P.D., Morris N.J.;
Mouse vp20/RIN4C cDNA.";
                                                                                                                                                                                                                                                                       35 ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF02453; Reticulon; 1.
PROSITE; PS50845; RETICULON; 1.
 InterPro; IPR003388; Reticulon.
                                                                                        52.7%;
                                                                                                     Best Local Similarity 35.59
Matches 229; Conservative
                                           NON TER 1
SEQUENCE 658 AA;
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                                                                                        Query Match
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RTN4 MOUSE
DD RTN4 MOUSE
DD 28-FEB
DT 08-FEB
DT 05-JUL
DE RETICUL
GN NAME=RC
OC EUKATY
OC MAMMA1
OC MAMMA1
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RC STRAIN
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REALINES-22354683; PubMed=12466851; DOI=10.1038/nature01266; REALINES-22354683; PubMed=12466851; DOI=10.1038/nature01266; REALINES-22354683; PubMed=12466851; DOI=10.1038/nature01266; REALINES-22354683; PubMed=12466851; DOI=10.1038/nature01266; REALINES-22354683; PubMed=12466851; DOI=10.1038/nature01266; REALINES-2354683; PubMed=12466851; DOI=10.1038/nature01126; Realine I., Ranapin A., Ranapin A., Ranapin A., Ranapin A., Ranapin A., Ranapin A., Ranapin A., Ratcher C.F., Forrest A., Frazer K.S., Baldarellia E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., R.A. Gastincich S., Hirokawa N., Jackson I.J., Jarvis E.D., Ranai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Konagaya A., Kurochkin I.V., Lee Y., Lehhard B., Lyons P.A., Ronagaya A., Kurochkin I.V., Lee Y., Lehhard B.L., Miki H., Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi. D., Ramachandran S., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Nanshaw-Boris A., Yanagisawa M., Yang I., Yang I., Yang I., Yang I., Yang I., Yang I., Wahlestedt C., Wang Y., Watanabe Y., Walsan M., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sakazume N., Sakazume N., Sakazime N., Hashizume W., Inderani K., Ishii Y., Itoh M., Kagawa I., Ranayasaki A., Sakai K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Raminyasaki A., Sakai K., Sasaki D., Shinagawa A., Haraki K., Rawai J., Aizawa K., Lander E.S., Rogers J., R., Mallygis of the mouse transcriptome based on functional annotation of K. Wana L., Allanger L., While M., Malayasaki A., Sakai K., Sasaki D., Shinagawa G., Chullellength Chullellength Chullellength Chullellength Chullellength Chullellength Chullellength Chullellength Chullellength Chullellength Chullellength Chullellength Chullellength Chullellength Chullellength Chullellength Chullellength Chullellength Chullellength Chullellength Chulle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Potent neurite outgrowth inhibitor which may also help block the regeneration of the nervous central system in adults (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AK003859; AMNOTATED_CDS.

EMBL; AK003859; -1, NOT ANNOTATED_CDS.

MGD; MGI:1915835; Rtn4.

MGD; MGI:1915835; Rtn4.

MGD; MGI:1915835; C:endoplasmic reticulum membrane; ISS.

GO; GO:00010176; C:integral to endoplasmic reticulum membrane; ISS.

GO; GO:0005515; C:integral to endoplasmic reticulum membrane; ISS.

GO; GO:0019887; P:negative regulation of anti-apoptosis; ISS.

GO; GO:0010517; P:negative regulation of axon extension; ISS.

GO; GO:0007399; P:neurogenesis; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity).
SUBCELLULAR LOCATION: Integral membrane protein. Anchored to
membrane of the endoplasmic reticulum through 2 putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity).
SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSÍTE; PS50845; RETICULON; 1.
Alternative splicing; Endoplasmic reticulum; Transmembrane.
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytoplasmic (Potential). Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event-Alternative splicing, Named isoforms=1;
Comment=A number of isoforms may be produced;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: Contains 1 reticulon domain.
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PROSITE; PS50845; RETICULON; 1.
                           [2]
SEQUENCE OF 170-199 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF326337; AAK08076.1;
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133 DDEPPARPPPPAGASPLAEPAAPPSTPAAPKRRGSGSSVVDLLYWRDIKKTGVVFGAS 192
                                                                                                                                                                                                                                      193 LFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAIS 252
                                                                                                                                                                                                                                                                                                         EBLVOKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILA 312
                                                                                                                                                                                                                                                                                                                            92 EELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMMYFTYVGALFNGLTLLILA 151
                                                                                                                                                                                          32 LFLLLSLTVFSIVSVTAXIALALLSVTISFRIYKGVIQAIQKSDEGHPPRAYLESEVAIS 91
                                                                                                   Ouery Match 50.1%; Score 914; DB 1; Length 199;
Best Local Similarity 83.3%; Pred. No. 1.2e-22;
Matches 190; Conservative 3; Mismatches 5; Indels 30; Gaps
                                                                                                                                                                                                                                                                                                                                                                                              137 Lumenal (Potential).
162 Potential.
199 Cytoplaamic (Potential).
199 Reticulon.
22466 MW; 07BESDS80059ED9C CRC64;
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                                                                     199 AA;
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SEQUENCE
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882.327 Million cell updates/sec
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1850
1 MEDLDQSPLVSSSDSPPRPQ......VKDAWAKIQAKIPGLKRKAE 361
                                                                                                                                                June 23, 2005, 09:47:53; Search time 30.5423 Seconds
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                             513545 seqs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                  OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
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Result No.	Score	Query	Query Match Length	DB	ID	Description
1	927	50.1	-	2	US-08-700-607-1	Sequence 1. Appli
6	927	50.1	. 201	4	US-09-949-016-9124	915
٣	827.7	44.7	176	~	US-08-700-607-5	
4	827.7	44.7	176	4	9	69
S	804.9	43.5	439	4	US-09-949-016-9180	918
9	789.8	42.7	356	7	US-08-700-607-6	6, App
7	684.2	37.0	208	~	US-08-700-607-7	7
80	999	36.0	267	7	US-08-700-607-8	Sequence 8, Appli
6	627.9	33.9	192	4	US-09-949-016-8859	885
10	599.1	32.4	588	4	US-09-949-016-7290	Sequence 7290, Ap
11	541.9	29.3	168	4	US-09-149-476-563	a.
12	538.3	29.1	241	~	US-08-700-607-3	۳ ک
13	518	28.0	219	4	US-09-270-767-45132	45
14	348.9	18.9		4	US-09-621-976-4600	Sequence 4600, Ap
15	348.9	18.9	75	4	US-09-621-976-4601	Sequence 4601, Ap
16	347	18.8	9	4	US-09-513-999C-6304	Sequence 6304, Ap
17	285	15.4		4	US-09-149-476-411	Sequence 411, App
18	276.2	14.9	1027	4	US-09-902-540-11750	1175
19	259.7	14.0		~	US-09-080-897-2	7
20	259.7	14.0		ო	US-09-323-735-2	Sequence 2, Appli
21	258.2	٠		m	US-08-899-595-3	θ,
22	256.5	13.9		~	US-09-080-897-4	4
23	256.5	13.9		ო	US-08-899-595-1	H
24	256.5	13.9		ო	US-09-323-735-4	Sequence 4, Appli
25	248.2	13.4	114	4	US-09-513-999C-7861	786
26	247	13.4	2090	4	US-09-538-092-1081	1081,
27	247	13.4	2120	4	118-09-949-016-9768	9768

Sequence 32, Appl	Sequence 22, Appl	Sequence 2, Appli	Sequence 10562, A	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 14, Appl	Sequence 14, Appl	Sequence 11382, A	Sequence 11383, A	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli
US-08-714-741-32	US-08-922-635-22	US-09-364-206-2	US-09-949-016-10562	US-08-459-568-4	US-08-399-411-4	· US-08-516-859A-4	US-09-586-472-4	US-09-528-706-4	US-08-764-870-14	US-08-980-115-14	US-09-949-016-11382	US-09-949-016-11383	US-08-459-568-2	US-08-399-411-2	US-08-516-859A-2	US-09-586-472-2	US-09-528-706-2
4	m	4	4	N	C*	n	m	4	m	ო	4	4	7	N	m	m	4
8991	1070	1504	990	1719	1719	1719	1719	1719	933	933	1540	1540	1706	1706	1706	1706	1706
13.3	13.3	13.3	13.2	13.2	13.2	13.2	13.2	13.2	13.1	13.1	12.9	12.9	12.9	12.9	12.9	12.9	12.9
246.1	245.8	245.8	244.5	243.6	243.6	243.6	243.6	243.6	241.5	241.5	238.7	238.7	238.7	238.7	238.7	238.7	238.7
28	. 29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Gaps
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                         GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                       3: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ Version 1.5 SOFTWARET APPLICATION UNDER: US/08/700,607 FILING DATE: Filed Herewith ATTORNEY/AGENT INFORMATION:
; Sequence 1, Application US/08700607; Patent No. 5858708
                                                                                                                                                                                                                                                                    COUNTY.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: PI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    199 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Billings, Lucy J
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0
Matches 188; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         415-845-4166
                                                                                                                                                                                                          STREET: 3174 Port
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
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IMMEDIATE SOURCE:
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174 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 233

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; Pred. No. 3.6e-28;
55; Mismatches 89;
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  CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                   MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 1.5
CURRENT APPLICATION UNDER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    PF-0114 US
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                                                                                                                                                                                                                                                                                                                                      NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-TELECOMMUNICATION INFORMATION: 415-855-0555
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                                           STREET: 3174 Porter Drive
CITY: Palo Alto
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Matches 196; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIBRARY: GenBank
CLONE: 307307
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                                                                 CITY: Pa
STATE: C
COUNTRY:
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR PELING DATE: 2000-10-03
PRIOR PELING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 9124
LENGTH: 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 193
                                                                 234 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 293
                                                                                         72 OKSDEGHPPRAYLESEVAISEELVOKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 131
                                                                                                                                                 294 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 353
                                                                                                                                                                           132 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 293
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                       71
12 VVDLYWRDIKKTGVVFGASLFLLLSLIVFSIVSVTAYIALALLSVTISFRIYKGVIQAI
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APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.1%; Score 927; DB 4; L
100.0%; Pred. No. 1.1e-33;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/08700607
Patent No. S858708
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.(
Matches 188; Conservative
                                                                                                                                                                                                                                                                         PGLKRKAE 199
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PGLKRKAE 201
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Db 427 LPSGYVSFGHVGGPPPSPASPSIQYSILREEREAELDSELIIESCDASSASEESPK 482 104 RQPSWDPSPVS	QY 299 YVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKR 358 Db 714 YVGALFNGLTLLLMAVVSMFTLPVVYVKHQAQIDQYLGLVRTHINAVVAKIQAKIPGAKR 773 QY 359 KAE 361 Db 774 HAE 776 RESULT 5 18 RESULT 5	US-09-949-016-9180, Application US/09949016 ; Sequence 9180, Application US/09949016 ; Patent No. 6812339 ; GENERAL INFORMATION: ; PAPPLICANT: VENTER, J. Craig et al. ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF; ; TILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF; ; CURRENT APPLICATION NUMBER: US/09/949,016 ; CURRENT FILING DATE: 2000-04-14 ; PRIOR FILING DATE: 2000-10-20 ; PRIOR FILING DATE: 2000-10-20 ; PRIOR FILING DATE: 2000-10-20 ; PRIOR FILING DATE: 2000-10-20	FRIOR FPILING NUMBER: 60/231,498	Query Match 43.5%; Score 804.9; DB 4; Length 439; Best Local Similarity 40.9%; Pred. No. 1.2e-27; Matches 177; Conservative 48; Mismatches 97; Indels 111; Gaps 11; Qy 4 LDQSPLVSSSDSPPRQPAFKYQFVERPEDEBEBEBEBEBEBEBEBEBEBEBEBEBEBEBEBEBEBE	64 SAAPVPTAPAAGAPLMDFCNDFVPPAPRGPLPAAPPV
Qy 179 YWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDE 238 Db 594 YWRDIKQTGIVFGSFLLLLFPSLTQFSVVSVVAXLALAALSATISFRIYKSVLQAVQKTDE 653 Qy 239 GHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMWVFT 298 Db 654 GHPFRAYLELEITLSQEQIQKYTDCLQFYVNSTLKELRRLFLVQDLVDSLKFAVLMMLLT 713 Cy 299 YVGALFNGLTLLIALISLESVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKR 358 Db 714 YVGALFNGLTLLLALISLESVPVIYERHQAQIDQYLGLVRTHINAVAKIQAKIPGAKR 773 Cy 359 KAE 361 Db 774 HAE 776	ation US/09 Craig et POLYMORPHIS WITH HUMAN 1307 NUMBER: US/	PRIOR APPLICATION NUMBER: 60/241,755	Query Match 44.7%; Score 827.7; DB 4; Length 776; Best Local Similarity 27.1%; Pred. No. 3.6e-28; Indels 383; Gaps Matches 196; Conservative 55; Mismatches 89; Indels 383; Gaps 6 QSPL	10VSSSDSPRPQP	QY 51 53 Db 250 IXDHLLEESTFAPY1DDLSEEQRRAPQITTPVKITLTEIEPSVETTTQEKTPEKQDICLK 309 QY 54

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200 VVSVVAYLALAALSATISFRIYKSVLQAVQKTDEGHPFKAYLELEITLSQEQIQKYTDCL 259
                                                                                                                                                                                                                                                    260 QFYVNSTLKELRLRLPLVQDLVDSLKFAVLMMLLTYVGALFNGLTLLLMAVVSMFTLPVVY 319
                                      89 RAPSRRGLAEPGSFLDYPSTEPOPGP-----ELPPGDGALEPETPMLPRKPEEDSS 139
  104 ROPS----WDPS---PVSSTVPAPSPLSAAAVSPSKLPEDD-----EPPARPPPPPASV 151
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                                                                                                 152 SPQAEPVWTPPAP-APAAPP----STSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFS
                                                                                                                                                                                                                                    265 LGHVNCTIKELRRIFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          152 SPQAEPVWTPPAPAPPAPPSTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSTVSVTAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 208;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Au-Young, Janice
APPLICANT: Al-Young, Janice
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                       320 VKHQAQIDQYLGLVRTHINAVVAKIQAKIPGAKRHAE 356
                                                                                                                                                                                                                                                                                                               325 ERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 37.0%; Score 684.2; DB 2; Best Local Similarity 62.4%; Pred. No. 6.7e-23; Matches 131; Conservative 35; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: DOS
SOFTWARE: FastSEO Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0114 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/08700607
Patent No. 5858708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 208 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Dioter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SS: single
linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: lines
MOLECULE TYPE: po
IMMEDIATE SOURCE:
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CITY: Pa
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                                                                                247 INKQKAIDLLYWEDIKQTGIVFGSFLLLLFSLTQFSVVSVVAYLALAALSATISFRIYKS 306
                                                                                                                                       KFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK 348
                                                                                                                                                         229 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSL 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 PPRP-OPAFKYOFVREPEDEE-------EEEEEEEEEDEDEDLEELEVLERK 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 112;
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                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Au-Young, Janice
APPLICANT: Oli, Surya K.
APPLICANT: Hilman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 PPSPASPSIQYSILRĒEREAĒLDSELIIESCDASSASĒĒSPKRĒQD
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Pred. No. 3.9e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette
COMPUTER: IEM COMPAILSE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATORNESY/AGENT INFORMATION:
NAME: Billings, Lucy J:
NAME: Billings, Lucy J:
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: PF-0114 US
TELECOMMUNICATION INPORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/08700607
Patent No. 5858708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 356 amino acids
TYPE: amino acid
STRANDEDNES: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                      427 İQAKİPGAKRHAE 439
                                                                                                                                                                                                                  349 IQAKIPGLKRKAE 361
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Best Local Similarity 42.6'
Matches 169; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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LIBRARY: Geneur
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ZIP: 94304
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US-08-700-607-6
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US-08-700-607-6
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Sequence 7290, Application US/09949016

Patent No. 6812339
GENERAL INPOWARTION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-06-08
NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER: FASE DE DIO NOS: 207012
SOFTWARE: FASES FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: WENTER, J. Craig et al.

APPLICANT: WENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-041,755

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-00-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastesQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      233 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   293 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 352
130 VLMWLLTYVGALFNGLTLLLLMAVVSMFTLPVVYVKHQAQVDQYLGLVRTHINTVVAKIQA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 SVHDLIFWRDVKKTGFVFGTTLIMLLSLAAFSVISVVSYLILALLSVTISFRIYKSVIQA 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.9%; Score 627.9; DB 4;
61.1%; Pred. No. 1.8e-20;
tive 38; Mismatches 35;
                                                                                                                                                                                                                                                                                                            ; Sequence 8859, Application US/09949016; Patent No. 6812339; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.94
Query Match
Best Local Similarity 61.14
Matches 116; Conservative
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183 LPGIAKKKAE 192
                                                                  352 KIPGLK 357
                                                                                                                                         190 KIPGAR 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 8859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     292 VLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQA 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 SQAIDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVVSVVAYLALAALSATISFRIYKSVLQ 69
                             212 IALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCT
                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/08700607
; Sequence 8, Application US/08700607
; Patent No. S858708
; GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Jannice
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 267;
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                                                                                                                                                                                                                                                                                                                                                            DHYLGLANKNVKDAMAKIQAKIPGLKRKAE 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 36.0%; Score 666; DB Best Local Similarity 66.1%; Pred. No. 6.8e Matches 123; Conservative 34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMFUTER: SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAMME: Billings, Lucy J.
REGISTRATION NUMBER: PF-0114 US
TELEPHONE: 415-85-055
TELEPHONE: 415-85-055
TELEPHONE: 415-85-055
TELEPHONE: 415-85-055
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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COMPUTER READABLE FORM:
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76 DFRELHTAREFSEBDEBETTSQDWGTPRELTFSYIAFDGVVGSGGRRDSTARRFRPQGRS 135
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                                                                                                                                                                                                                                                                                   ; Score 599.1; DB 4; Length 588;
; Pred. No. 2.8e-18;
56; Mismatches 122; Indels 249; Gaps
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R FILING DATE: 1997-03-07
R APPLICATION NUMBER: 60/040,626
R FILING DATE: 1997-03-07
R FILING DATE: 1997-03-07
R FILING DATE: 1997-03-07
R APPLICATION NUMBER: 60/040,336
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Patent No. 6420526
GENERAL INFORMATION:
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26.9%;
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Best Local Similarity 26.9
Matches 157; Conservative
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; LENGTH: 588
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7290
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US-09-149-476-563
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APPLICATION NUMBER: 60/047,581
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APPLICATION NUMBER: 60/047,582
APPLICATION NUMBER: 60/047,582
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APPLICATION NUMBER: 60/047,615
FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,584
FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,612
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APPLICATION NUMBER: 60/043,580
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APPLICATION NUMBER: 60/043,669
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FILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/043,315
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/040,163
FILING DATE: 1997-03-07
                                   APPLICATION NUMBER: 60/047,600
FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,583
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FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
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R APPLICATION NUMBER: 60/056,880
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,894
R PILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,911
R PILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,636
R PILING DATE: 1997-08-22
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R APPLICATION NUMBER: 60/056,893
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,630
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,878
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R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/047,595
R FILING DATE: 1997-08-23
R APPLICATION NUMBER: 60/047,599
R FILING DATE: 1997-05-23
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R APPLICATION NUMBER: 60/047,586
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R APPLICATION NUMBER: 60/047,590
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R APPLICATION NUMBER: 60/056,864

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,631

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,845

R APPLICATION NUMBER: 60/056,845

R APPLICATION NUMBER: 60/056,892

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R APPLICATION NUMBER: 60/047,589

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R APPLICATION NUMBER: 60/047,614
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APPLICATION NUMBER: 60/056,889
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,888
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,886
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FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/056,882
                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/056,637
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FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/043,576
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APPLICATION NUMBER: 60/047,501
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                 1997-08-2
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61 APHNYMAAAMVHINRALKLIIRLFLVEDLVDSLKLAVFMWLMTYVGAVFNGITLLILAEL 120
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; Pred. No. 8.9e-17;
34; Mismatches 31; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 316 SLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGL-KRKAE 361
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EARLIER FILING DATE: 1997-04-11
EARLIER FILING DATE: 1997-04-12
EARLIER FILING DATE: 1997-04-22
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,664
EARLIER PILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,862
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EARLIER APPLICATION NUMBER: 60/056,862
EARLIER APPLICATION NUMBER: 60/056,862
EARLIER PILING DATE: 1997-08-22
EARLIER PILING DATE: 1997-08-22
EARLIER PILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-06-66
EARLIER FILING DATE: 1997-08-26
EARLIER FILING DATE: 1997-08-26
EARLIER RELING DATE: 1997-08-66
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-08-22
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EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02
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Patent No. 5858708
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Best Local Similarity 60.5*
Matches 101, Conservative
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GENERAL INFORMATION:

APPLICANT: Bandman, Olga
APPLICANT: Au-Young, Janice
APPLICANT: All-Young, Janice
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: HILLMAN, Jennifer L.
APPLICANT: HILLMAN, Jennifer L.
APPLICANT: HILLMAN, Jennifer L.
APPLICANT: HILLMAN, Jennifer PROTEINS
NUMBER OF SEQUENCES:
ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA COUNTRY: U.S.

IBM Compatible

ZIP: 94304 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Con OPERATING SYSTEM:

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Query Match
Best Local Similarity 51.4%;
Matches 95; Conservative 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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LOCATION: 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 AAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAPAP-----STSVVD 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                177 LLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRIFLVDDLVDSLKFAVLMWV 296
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Retent No. 6703491

GENERAL INFORMATION

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REPERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 45132

LENGTH: 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 167; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               29.1%; Score 538.3; DB 2; Length 241; 30.9%; Pred. No. 2.6e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38; Mismatches
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0114 US
TELECHONE: 415-845-0555
TELECHONE: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT; ORGANISM: Drosophila melanogaster US-09-270-767-45132
                                                                                                                                                                           TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 30.9<sup>3</sup>
Matches 112; Conservative
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IMMEDIATE SOURCE:
LIBRARY: THPINOB01
CLONE: 31870
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US-09-270-767-45132
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FTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGL 356
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                                                                                           177 LLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKS
                                                 Gaps
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; Score 518; DB 4; Length 219;
; Pred. No. 1.7e-15;
42; Mismatches 48; Indels
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Sequence 4600, Application US/09621976

Patent No. 6639063

GENERAL INFORMATION:
APPLICANT: Undert, S.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GRNSET: 054PR2
CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm
LENGTH: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
18.9%; Score 348.9; DB 4.
Best Local Similarity 82.6%; Pred. No. 6.8e-09;
Matches 71; Conservative 0; Mismatches 4.
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US-09-621-976-4601
Sequence 4601, Application US/09621976
Parent No. 6639063
GENERAL INFORMATION:
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OTHER INFORMATION: Xaa = His, Pro
NAME/KEY: UNSURE
LOCATION: 28
OTHER INFORMATION: Xaa = Met, Val
NAME/KEY: UNSURE
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US-09-621-976-4600
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Search completed: June 23, 2005, 10:17:49 Job time: 32.5423 secs

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Sequence 20, Appl Sequence 10, Appl Sequence 18, Appl Sequence 10, Appl Sequence 10, Appl Sequence 21, Appl Sequence 25, Appl Sequence 25, Appl Sequence 26, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl

Sequence 23, A Sequence 7, Ap Sequence 164,

Sequence 9

Sequence 21, Appl Sequence 11, Appl Sequence 5, Appli Sequence 430, App Sequence 1481, Ap Sequence 93, Appl Sequence 6, Appli Sequence 6, Appli

Sequence 2892, Ap Sequence 2330, Ap Sequence 127, App

Sequence 8, Appli

61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120

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Result Š. 9

Gaps

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Sequence:

Run on:

Searched:

Database

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1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEEEEEEEEEEELEVLERKPA
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APPLICANT: MICHALOVICH, DAVID
APPLICANT: MICHALOVICH, DAVID
APPLICANT: MICHALOVICH, DAVID
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP-30165-C1
CURRENT FILING DATE: 2001-02-21
FRIOR APPLICATION NUMBER: U.K. 9916898.1
PRIOR FILING DATE: 1999-07-19
PRIOR APPLICATION NUMBER: U.K. 9916898.1
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 1999-07-22
NUMBER OF SEQ ID NOS: 6
SEQ ID NOS: 6
SEQ ID NOS: 6
SEQ ID NOS: 6
SEQ ID NOS: 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 6, Application US/09789386; Patent No. US20020010324A1; GENERAL INFORMATION:
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Matches 360; Conservative
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Sequence 8, Appli
Sequence 24, Appli
Sequence 6, Appli
Sequence 2, Appli
Sequence 6, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 23, Appli
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1271.831 Million cell updates/sec
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Sequence 6, Appli
Sequence 24, Appl
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                                                                                                                                                                                                                                                                                         .....VKDAMAKIQAKIPGLKRKAE 361
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                                                                                                                                                 June 23, 2005, 09:56:59 ; Search time 109.151 Seconds
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_MEW_PUB_pep:*
4: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB_pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB_pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB_pep:*
6: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB_pep:*
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9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
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21: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
22: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
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US-10-810-633-24
US-10-347-669-6
US-10-46-258-4
US-09-789-386-2
US-09-788-140-6
US-09-893-348-23
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US-09-765-205-6
US-09-893-348-24
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.1
                                                                                                                                                                                                                                                                                     1 MEDLDQSPLVSSSDSPPRPQ
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Maximum DB seq length: 2000000000
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Match Length
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Perfect score:
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Pred. No. 9.1e-56;
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GENERAL INFORMATION: APPLICANT: Benson, Darin R.
                                                                                          Sequence 24, Application US/09893348
Patent No. US20020072493A1
GENERAL INFORMATION:
APPLICANT: EISENBACH-SCHWARTZ, Miche
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Best Local Similarity 96.5%;
Matches 360; Conservative
361 IQAKIPGLKRKAE 373
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Best Local Similarity
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                                                                  121 SPLSAAAVSPSKLPEDDEPPARPPPPPASVSPQAEPVWTPPAPAPAAPSTRPAAPKRRG 180
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                                                                                                                                181 SSGSVVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG
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                                                SPLSAAAVSPSKLPEDDEPPARPPPPASVSPQAEPVWTPPAPAPAPPSTS-----
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APPLICANT: Cao, Li
TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
FILE REFERENCE: 1458.004/200130.449
CURRENT APPLICATION NUMBER: US/09/765,205
CURRENT FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US/09/212,440
PRIOR PLING DATE: 1998-12-16
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FRALESEQ for Windows Version 3.0
SEQ ID NO 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12;
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Patent No. US20020034800A1
                                                                                                                                                                                                                                                                                                           IQAKIPGLKRKAE 361
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TYPE: PRT
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US-09-765-205-6
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APPLICANT: COHEN, ITUM R.
APPLICANT: COHEN, ITUM R.
APPLICANT: COHEN, ITUM R.
APPLICANT: BESERMAN, Pierre
APPLICANT: MOSCNEGO, Alon
APPLICANT: MOALEM, Gila
ITILE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR US)
FILE REPERRORE: BIS-SCHWARTE-2A
CURRENT PELLOGATION NUMBER: US 09/893,348
CURRENT FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: US 09/314,161
PRIOR PELING DATE: 1999-05-19
PRIOR FILING DATE: 1998-12-22
PRIOR PELING DATE: 1998-12-22
PRIOR PELING DATE: 1998-05-19
PRIOR FILING DATE: 1998-05-19
PRIOR FILING DATE: 1998-05-19
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn Version 3.1
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APPLICANT: ESSERMAN, Pierre
APPLICANT: COHEN, Irun R.
APPLICANT: COHEN, Irun R.
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR US
FILE REPERBUCE: EIS-SCHWARTZ=2A
CURRENT FILING DATE: 2004-03-29
PRIOR APPLICATION NUMBER: US/09/893,348
PRIOR PLING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: US 09/314,161
PRIOR APPLICATION NUMBER: US 09/314,161
PRIOR APPLICATION NUMBER: US 09/314,161
PRIOR PILING DATE: 1998-12-22
PRIOR FILING DATE: 1998-12-22
PRIOR FILING DATE: 1998-12-22
PRIOR FILING DATE: 1998-05-19
PRIOR SPELING DATE: 1998-05-19
PRIOR SPELING DATE: 1998-05-19
PRIOR SEQ ID NOS: 29
NUMBER OF SEQ ID NOS: 29
NUMBER OF SEQ ID NOS: 29
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                       1; Indels
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                         Mismatches
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Best Local Similarity 96.5:
Matches 360; Conservative
                       Matches 360; Conservative
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Publication No. US20040063161A1
GENERAL INFORMATION:
APPLICANT: Pharmacia & Upjohn Company
APPLICANT: Yan, Rigiang
APPLICANT: Lu, Yifeng
TITLE OF INVENTION: Compositions and Methods of Treating Alzheimer's Disease
FILE REFERENCE: 00925
CURRENT APPLICATION NUMBER: US/10/408,967
CURRENT FILING DATE: 2003-04-08
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
LENGTH: 373
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Pred. No. 9.1e-56;
0; Mismatches 1; Indels 12; Gaps
APPLICANT: Kalos, Michael D.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Persing, David H.
APPLICANT: Hepler, William T.
APPLICANT: Jiang, Yuqiu
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REFERENCE: 21012.56
CURRENT APPLICATION NUMBER: US/10/060,036
CURRENT FILING DATE: 2002-01-30
NUMBER OF SEQ ID NOS: 4560
SOFTWARE: PSELSEQ for Windows Version 4.0
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Pred. No. 9.1e-56;
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96.5%;
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Best Local Similarity 96.5%;
Matches 360; Conservative (
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                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
US-10-060-036-72
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CRGANISM: Homo sapiens
US-10-408-967-8
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Best Local Similarity
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US-10-408-967-8
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Pred. No. 1.7e-55;
1; Mismatches 2;
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Fatent No. US20020010324A1
GRNEAL INFORMATION:
GRNEAL INFORMATION:
TITLE OF INVENDING, RABINDER KUWAR
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REPERBNCE: GP-30165-C1
CURRENT APPLICATION NUMBER: US/09/789,386
CURRENT FILING DATE: 2001-02-21
PRIOR PELLON NUMBER: U.K. 9916898.1
PRIOR PELLING DATE: 1999-07-19
PRIOR PELLING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: US 09/359,208
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: US 09/359,208
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 1999-07-22
SPRIOR FILING DATE: 1999-07-22
                                                                                                                                                                                                  APPLICANT: GLAXO GROUP LIMITED
TITLE OF INVENTION: ASSAY
FILE REFERENCE: P80966 GCW
CURRENT APPLICATION NUMBER: US/10/466,258
CURRENT FILING DATE: 2003-07-15
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.0
                                                                                                                             Sequence 4, Application US/10466258
Publication No. US20040132096A1
GENERAL INFORMATION:
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96.0%;
     361 IQAKIPGLKRKAE 373
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Matches 358; Conservative
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ORGANISM: Homo sapiens
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61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120
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TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
FILE REFERENCE: 1458 004/20130.449
CURRENT APPLICATION NUMBER: US/10/347,669
CURRENT FILING DATE: 2003-01-16
PRIOR FILING DATE: 1998-12-16
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FaelSEQ for Windows Version 3.0
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Pred. No. 9.16-56;
0; Mismatches 1; Indels 12;
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Publication No. US20050084850A1
GENERAL INFORMATION:
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Best Local Similarity 96.5%;
Matches 360; Conservative
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ORGANISM: human
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APPLICANT: Strittmatter, Stephen M.
TITLE OF INVENTION: No. US20020012965Alo Receptor-Mediated Blockade of Axonal Growt
FILE REPERENCE: 44574-5073-US
CURRENT APPLICATION NUMBER: US 60/175,140
CURRENT FILING DATE: 2001-01-12
PRIOR PILING DATE: 2000-01-12
PRIOR PLING DATE: 2000-01-12
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,366
PRIOR APPLICATION NUMBER: US 60/236,378
PRIOR FILING DATE: 2000-09-29
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3.2e-52;
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Pred. No. 3.2e-
0; Mismatches
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Best Local Similarity 30.3%;
Matches 361; Conservative
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SOFTWARE: PatentIn Ve
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                                                                                          Score 1756.9; DB 9; Length 1192;
Pred. No. 3.2e-52;
0; Mismatches 0; Indels 831; Gaps
                                                                                          95.0%;
30.3%;
                                                                                                         Best Local Similarity 30.3
Matches 361; Conservative
             LENGTH: 1192
TYPE: PRT
ORGANISM: HOMO SAPIENS
                                               , ORGANISM: HOUS-09-789-386-2
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SEQ ID NO 2
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PRIOR FILING DATE: 1998-07-21 PRIOR APPLICATION NUMBER: IL 124500	ING DAIE: 1998-0: SEQ ID NOS: 29 Datentin version	23 23	T. Homo good on	MAGANISM: MONIO BADIENB	95.0%; Score 1756.9;	LOCAL SIMILATILY 30.34; FIEG. NO. 3.26- es 361; Conservative 0; Mismatches	1 MEDLDQSPLVSSSDSPPRPQPAFKXQFVREPEDEEEEEEEEEEDDLEELEVLERKPA 60	1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEEEEEEEEEEEEEEEE	61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSFVSSTVPAP 120		121 SPLSAAAVSPSKLPEDDEPPARPPPPASVSPQAEPVWTPPAPAPAPAPS 171		172 171	181 SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP 240	172 171	241 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 300	172 171	301 GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHNQQELPTALTKLVKEDEVV 360	172 171	SSEKAKDSFNEKRVAVEAPMREEYADFKPFBRVWEVKDSKEDSDMLAAGGKIESNLESKV	172 171	421 DKKCFADSLEGTNHEKDSESSNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIATNIF 480	172 171	481 PLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTE 540	172 171	541 EVVANMPEGLIPDLVQEACESELNEVIGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF 600	172 171	601 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYE 660	172 171	661 EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE 720	172 171	721 MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMLVKESLTETSFESMI 780	172 171	781 BYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 840	172 171
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Ογ 172 171	Db 421 DKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF 480	Qy 172 171	Db 481 PLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTE 540	Qy 172 171	Db 541 EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF 600	Qy 172 171	Db 601 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYE 660	Qy 172 171	Db 661 BAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE 720	Qy 172 171	Db 721 MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMLVKESLTETSFESMI 780	Qy 172 171	Db 781 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 840	Qy 172 171	Db 841 SNDDLFISKEAQIRETETFSDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI 900	Qy 172 171	Db 901 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSALAT 960	Qy 172TSVVDLLYWRDIKKTGVV 189	Db 961 QAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGVV 1020	190	Db 1021 FGASLFLLLSLTVFSIVSVTAYIALALLSVTİSFRIYKGVIQAIQKSDEGHPFRAYLESE 1080	Qy 250 VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTL 309	Db 1081 VAISEELVQKYSNSALGHVNCTIKELRREFLVDDLVDSLKFAVLMWVFTYVGALFNGLTL 1140	Qy 310 LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 361	Db 1141 LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1192	טספודיה 11	NESCHI 11 VESCHI 12 VESCHI 12 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	93A1	; APPLICANT: ELEMENACH-SCHWARTZ, Michal	A PPLICANT: COLLEN, ILLIA K. ; APPLICANT: BESERMAN, PIETRE A ADDITOWNT: MOSONICO ALC	בובי ביבי ביביבים מוסייסים אוראנים אירינים אי	CCIIVALED I-CELES, NEKVOOS SISIEM-SFECIFIC ANIIGENS AND INEIK ICHWARTEZ 2A HTMPED: IIC/04/403 349	CORRENT AFFILTATION NOMBER: 05/03/03/340 CURRENT FILING DATE: 2001-06-28 PRIOR APPLICATION NUMBER: 17S 09/314.161	FIGURE FILLING DATE: 199-05-19 DETON ADDITIONATION NUMBER: 115 00/210 272	

Db 841 SNDDLFISKEAQIRETETFSDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI 900	Db 241 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 300
Qy 172 171	Qy 172 171
Db 901 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSALAT 960	Db 301 GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHNQQELPTALTKLVKEDEVV 360
Qy 172Qy 189	Qy 172 171
Db 961 QAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGVV 1020	Db 361 SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV 420
Oy 190 FGASLFLLLSLTVFSIVSVTAXIALASVTISFRIYKGVIQAIQKSDEGHPFRAYLESE 249	Ογ 172 171
Db 1021 FGASLFLLLSLTVPSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESE 1080	Db 421 DKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF 480
Qy 250 VAISEELVOKYSNSALGHVNCTIKELRREFLVDDLVDSLKRAVLMWVFTVGALFNGLTL 309	Qy 172 171
Db 1081 VAISBELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMMVFTYVGALFNGLTL 1140	Db 481 PLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTE 540
Qy 310 LILALISLESVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 361	Oy 172 171
Db 1141 LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1192	Db 541 EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF 600
RESULT 12	Qy 172 171
US-09-972-599A-6 ; Sequence 6, Application US/09972599A	Db 601 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYE 660
	Qy 172 171
; APPLICANT: STRITTMATTER, STEPHEN M	Db 661 BAMSVSLKKVSGIKEBEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE 720
FILE ROYALD AND TOTAL OF THE TOTAL THE THE THE THE THE THE THE THE THE THE	Qy 172 171
; CURRELL ALLICATION NOTION (0) 03/01/2/332A; CURRELL ALLICATION NATION (100/10/10/10/10/10/10/10/10/10/10/10/10/	Db 721 MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMLVKESLTETSFESMI 780
PRIOR PILLO DATE: 2001-01-12 PRIOR ADDITORNAL MARRED: 06/758 140	Qy 172 171
FRIOR FILING DATE: 2001-01-12 PRIOR PLING DATE: 2001-01-12	Db 781 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 840
; PRIOR APPLICATION NIMBER: 6//2013 36	Qy 172 171
PRIOR APPLICATION NUMBER: 60/175, 707	Db 841 SNDDLFISKEAQIRETETFSDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI 900
FRIOR FILING DATE: 2000-01-12 NIMBER OF SEO ID NOS: 57	Qy 172 171
S	Db 901 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSALAT 960
~	Qy 172TSVVDLLYWRDIKKTGVV 189
; ORGANISM: Homo sapiens US-09-972-599A-6	Db 961 QAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGVV 1020
Query Match 95.0%; Score 1756.9; DB 9; Length 1192; Best Local Similarity 30.3%; Pred. No. 3.28-52; Matches 361: Conservative 0. Mismatches 0. Indels 831. Gans 1.	Qy 190 PGASLPLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDBGHPFRAYLESE 249
VSSSPPRPQPAFKYQFVRENEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE	Oy 250 VAISEBLVOKKSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTL 309
Db 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEBEBEBEBEBEBEBEBEBEBEBEBEBEBEBEBEBEB	דרסיד איניסיייייייייייייייייייייייייייייייייי
Qy 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPARRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120 Db 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPARGPLPAAPPVAPERQPSWDPSPVSSTVFAP 120	OY 310 LILALISLESVPVIYERHQAQIDHYLGLANKNVKDAWAKIQAKIPGLKKKAE 361
Qy 121 SPLSAAAVSPSKLPEDDEPPARPPRSVSPQAEPVWTPFAPAPAAPPS 171	RESULT 13 US-10-060-036-71 ; Sequence 71, Application US/10060036
Qy 172 171	; Publication No. US20030073144A1 ; GENERAL INFORMATION:
Db 181 SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP 240	; APPLICANT: Bengoh, Darin K. ; APPLICANT: Kalos, Michael D. ; APPLICANT: Lodes. Michael J.
Qy 172 171	; APPLICANT: Persing, David H. ; APPLICANT: Hepler, William T.

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95.0%;
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Matches 361; Conservative
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ORGANISM: Homo sapiens
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US-10-267-502-429
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                                                                                                                                                                                                               Gaps
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APPLICANT: Jiang, Yuqiu
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REFERENCE: 21012.1.65
CURRENT APPLICATION NUMBER: US/10/060,036
CURRENT FILING DATE: 2002-01-30
NUMBER OF SEQ ID NOS: 4560
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 71
LENGTH: 1192
                                                                                                                                                                                    Score 1756.9; DB 14
Pred. No. 3.2e-52;
0; Mismatches 0;
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Best Local Similarity 30.3%;
Matches 361; Conservative
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Pred. No. 3.2e-52;
); Mismatches 0; I
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Publication No. US20040071700A1
GENERAL INFORMATION:
GENERAL INFORMATION:
FULL OF INVENTION: Galant, Ron
TITLE OF INVENTION: Obesity Linked Genes
FILE REFERENCE: LD5-07416
CURRENT APPLICATION NUMBER: US/10/267,502
CURRENT FILING DATE: 2003-01-27
NUMBER OF SEQ ID NOS: 439
SEQ ID NO 429
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; LENGTH: 1192 ; TYPE: PRT ; ORGANISM: Homo sapiens	•	Matches 361	Qy 1 MEDLDQSPLVSSDSPPRI	-	61	61		121	172		172		172	301	172		172		172		172	_	172		172		Dh 721 MAKWEODVDHSELVEDS	172	Db 781 EYENKEKLSALPPEGGKPY	Ογ 172	DD 841 SNDDLFISKEAQIRETETE	Oy 172	Db 901 ANAPDGAGSLPCTELPHDI
172 171 361 SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV 420	2 171 1 DKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIATNIF 480	.2 171	11 PLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTE 540	.2 171	.1 EVVANMPEGLTPDI.VQEACESELNEVTGTKIAXETKMDI.VQTSEVMQESLYPAAQLCPSF 600	2 171	1 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYE 660	2 171	1 EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE 720	2 171	1 MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMLVKESLTETSFESMI 780	2 171	1. EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 840	2 171	1 SNDDLFISKEAQIRETETFSDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI 900	2 171	1 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSALAT 960	2TSWWDLLYWRDIKKTGWV 189	QAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELS	FGASL		VAISE		o LinaLi	LILALI		3-9 . Amplication US/10327213	; Publication No. US20040121341A1 ; GENERAL INFORMATION:	: FILBIN, MARIE T. : DOMENICONI, MARCO	INVENTION: INHIBITORS OF MYELIN-ASSOCIATED GLYCOPROTEIN (MAG)	SOLALING NEUKAL	FELLATION NUMBER: US/10/32/,213 TILING DATE: 2002-12-20 SEO ID NOS: 43	Patentin Ver. 2.1
96 Dp 36	Qy 172 Db 421	Qy 17:	Db 481	Qy 172	Db 541	Qy 172	Db 601	0y 172	Db 661	Oy 172	Db 721	Qy 172	Db 781	Qy 172	Db 841	Oy 172	Db 901	Qy 172	Db 961	Qy 190	Db 1021	Qy 250	Db 1081	Qy 31	Db 1141	E	KESOLI IS US-10-327-213-9 : Sequence 9. A	; Publication; GENERAL IN	, APPLICANT , APPLICANT	; TITLE OF	; FILE REF	CURRENT FILING DAY	SOFTWARE

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LLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120
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Score 1756.9; DB 16; Length 1192;
Pred. No. 3.2e-52;
0; Mismatches 0; Indels 831; Gaps
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TSVVDLLYWRDIKKTGVV 189	961 QAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGVV 1020	190 FGASLPLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQALQKSDEGHPFRAYLESE 249	FILLISLITVESIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESE 1080	250 VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKRAVLMWVFTYVGALFNGLTL 309	1081 VAISEELVÕKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMMVFTYVGALFNGLTL 1140	310 LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 361	1141 LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1192	
172	961	190	1021	250	1081	310	1141	
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Search completed: June 23, 2005, 10:34:33 Job time: 114.151 secs

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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: June 23, 2005, 10:16:50; Search time I14.158 Seconds

(without alignments)
1223.045 Million cell updates/sec
Perfect score: 1850
Sequence: 1850
Sequence: 1 MEDLAQSPLVSSSDSPRPQ......VKDAWAKIQAKIPGLKRKAE 361
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.1
Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 2105692
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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se : A Geneseq 16Dec04:* 1: geneseqp1980s:* 2: geneseqp1990s:* 3: geneseqp200s:* 4: geneseqp2001s:* 5: geneseqp2003s:* 7: geneseqp2003s:* 8: geneseqp2004s:* 8: geneseqp2004s:* and is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

					SUMMARIES	
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Result	,	Query	:		:	
. NO.	Score	Match	Length DB	BB :	ID	Description
-	ന	6	373	м	S	Aay53624 A bone ma
7	1833.8	99.1	373	m	AAY56969	Aay56969 Human MAG
٣	1833.8	99.1	373	m	AAB24242	Aab24242 Human Nog
4	1833.8	99.1	373	4	AAB82350	Aab82350 Human NOG
S	1833.8	99.1	373	ß	AAM47954	Aam47954 Human RTN
9	1833.8	99.1	373	Ŋ	ABP68601	Abp68601 Human pan
7	1833.8	99.1	373	ហ	ABB81079	Human
80	1833.8	99.1	373	7	AD163044	Adi63044 Human apo
σ	1833.8	99.1	373	7	ADK67503	Adk67503 Human RTN
10	1833.8	99.1		æ	ADP67235	
11	1825.8	98.7	373	Ŋ	ABG30937	Human
12	1756.9	95.0		٣	AAY56967	Human
13	1756.9	95.0		4	AAB82349	Aab82349 Human NOG
14	1756.9	95.0		4	AAU04591	Human
15	1756.9	95.0	1192	'n	ABG30938	Human
16	1756.9	95.0		ហ	ABP68600	Human
17	1756.9	95.0	1192	ß	ABB81078	Human
18	1756.9	95.0		9	ABR59667	. Abr59667 Human Nog
19	1756.9	95.0	1192	æ	ADO08103	Human
20	1756.9	95.0		80	ADP45551	Human
21	1756.9	95.0	1192	æ	ADP67234	Human
22	1756.9	95.0	1192	œ	ADR13966	Human
23	1749.9	94.6	1192	7	ADK67502	Adk67502 Human RTN
24	1749.9	٠	1192	œ	ADO26400	
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379 361 359	360 360 1163	1163	1162	291 973 983 983
84.1 83.9 83.7 83.7	83.6 80.0 79.9	0.67 0.60 0.60 0.60	78.7	71.6 66.7 55.6 55.6
1556.2 1551.6 1549.3 1546.3	1546.3 1480.5 1478.8	1478.8 1478.8 1478.8 1476.8	14/5.2 1455.3 1441.2 1324.8	1324.8 1234.5 1028 1028
26 27 28 29	30 33 33	3 3 3 4 4 5 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	38 39 41	4 4 4 4 2 6 4 6

ALIGNMENTS

XX XX XX XX XX XX XX XX XX XX XX XX XX
AAY53622-43 restromal cells.

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to regulate hematopoiesis, and to treat myeloid or lymphoid cell
deficiencies. In addition, they may be used to support the growth and
proliferation of erythroid progenitor cells, and to treat various
anaemias. They can have colony stimulating factor (CSF) activity and can
be used to support the growth and proliferation of myeloid cells such as
granulocytes, monocytes or macrophages, to prevent or treat myelo-
suppression, to support the growth and proliferation of megakaryocytes
and platelets, thereby allowing prevention or treatment of platelet
cand platelets, thereby allowing prevention or treatment of platelet
conjunction with platelet transfusions, to treat stem cell disorders
conjunction with platelet transfusions, to treat stem cell disorders
conjunction with platelet transfusions, to treat stem cell disorders
conjunction with platelet transfusions, to treat stem cell disorders
conjunction with platelet transfusions, to treat stem cell disorders
conjunction with platelet transfusions, to treat stem cell disorders
conjunction with platelet transfusions, to treat stem cell disorders
conjunction with platelet transfusions, to treat stem cell disorders
conjunction with platelet transfusions, to treat stem cell disorders
conjunction with platelet transfusions, to treat stem cell compartment after irradiation or chemotherapy.
They can be used for growth or differentiation of bone, cartilage,
tendon, ligament, or nerve tissue, as well as for wound healing and
tissue repair and replacement, and in the treatment of burns, incisions
and ulcers, to induce cartilage and/or bone growth in circumstances where
bone is not normally formed and thus have an application in healing bone
for the control or differentiation or the platelet or properties and the base and thus have an application in healing bone
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neuroendocrine-specific protein. The MAGI protein can be expressed by standard recombinant methodology. The MAGI polypeptides, polynucleotides and antibodies are useful for treating diseases, including neuropathies, spinal injury, neuronal degeneration, neuromuscular disorders, psychiatric disorders and developmental disorders, cancer, stroke and inflammatory disorders. The polynucleotide is also useful for chromosome localization and for tissue expression studies. The present sequence

represents the human MAGI protein variant

The invention relates to human MAGI protein, which is similar to

Claim 2; Page 22; 35pp; English

Novel polypeptides related to neuroendocrine-specific proteins ar polynucleotides useful for diagnosis of various diseases and for treatment of cancer and neurological disorders.

(SMIK) SMITHKLINE BEECHAM PLC.

Michalovich D, Prinjha RK;

N-PSDB; AAZ56888

99GB-00016898

19-JUL-1999;

99WO-GB002360.

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Best Local Similarity 96.5
Matches 360; Conservative
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AAB24242 standard; protein; 373 AA.

AAB24242

AAB24242 ID AAB2 XX AC AAB2

MAGI protein; neuroendocrine-specific protein; neuropathy; human; spinal injury; neuronal degeneration; neuromuscular disorder; cancer; psychiatric disorder; developmental disorder; inflammatory disorder; stroke; cytostatic; cerebroprotective; neuroprotective; variant.

Homo sapiens

Human MAGI polypeptide variant. 25-APR-2000 (first entry)

standard; protein; 373 AA

AAY56969;

AAY56969

RESULT 2

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The present sequence is that of human NOGO-B. NOGO-B is a previously known splice variant of the human NOGO gene on chromosome 2p21. The invention relates to a novel splice variant, NOGO-C (see ABB82348). It provides NOGO-C polypeptides and polynucleotides, and methods for producing such polypeptides by recombinant techniques. Also disclosed are methods for utilising NOGO-C polypeptides and polynucleotides in the treatment of diseases including neuropathies, splinal injury, brain injury, stroke, neuronal degeneration, for example Alzheimer's disease and Parkinson's disease, neuromuscular disorders, psychiatric disorders and developmental disorders. Also provided are methods for identifying agonists and agonists for use in treating conditions associated with NOGO-C imbalance, and diagnostic assays for detecting diseases associated with inappropriate NOGO-C activity or levels
                            301 KFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOGO-B; human; chromosome 2p21; neuropathy; spinal injury; brain injury; stroke; neuronal degeneration; Alzheimer's disease; Parkinson's disease; neuromuscular disorder; psychiatric disorder; developmental disorder; neuroprotective; nootropic; neuroleptic; antiparkinsonian; cerebroprotective; neuroleptic; diagnosis; therapy.
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                                                                                                                            Human NOGO-B protein.
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                                                                                         Human; Nogo B; cell stress response; hyperphosphorylated; brain tumour; stress-phosphorylated endoplasmic reticulum protein; cytostatic; gene therapy; cell growth; cellular stress response; neuron growth; regulator of oxidative stress; inhibitor of neurite outgrowth; axon regeneration; diagnosis; cancer; identification.
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                                                Human Nogo B protein sequence SEQ ID NO:2.
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21-JUN-1999; 99US-0140331P.
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N-PSDB; ABV94681.
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                     AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; Page 11 (Disclosure); 27pp; Chinese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM47954 standard; protein; 373 AA.
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N-PSDB; ABA05903.
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Best Local Similarity
Matches 360; Conserv
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The invention relates to an isolated polynucleotide (I) comprising: (a) any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide and pancreatic tumor polypeptides, useful f
diagnosing, preventing and/or treating cancer, particularly pancreatic
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pancreas; cancer; gene therapy; vaccine; immunostimulant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2, SEQ ID NO 72; 300pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lodes MJ, Persing DH,
                                                                                                                                                                                                                                                                                                                                           2001US-0265305P.
2001US-0265682P.
2001US-0267568P.
2001US-0278651P.
2001US-0287112P.
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12-JUL-2001; 2001US-0305484P.
20-AUG-2001; 2001US-0313999P.
27-NOV-2001; 2001US-0333626P.
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12;

1; Indels

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Mosonego A;

Beserman P,

Cohen IR,

Hauben E,

Eisenbach-Schwartz M,

Moalem G;

WPI; 2002-607255/65.

N-PSDB; ABN86601

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RES & DEV

(YEDA) YEDA

98IL-00124500. 98WO-US014715. 98US-00218277. 99US-00314161.

21-JUL-1998; 22-DEC-1998; 19-MAY-1999;

19-MAY-1998;

2001US-00893348

Promoting nerve regeneration and preventing neuronal degeneration in central/peripheral nervous system from injury/disease, comprises administering nervous system-specific activated T cells/antigen, or

The invention relates to promoting nerve regeneration or conferring

Example; Page 56-57; 93pp; English.

analogs/peptides.

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complements of (a); (c) sequences consisting of at least 20 contiguous residues of (a); (d) sequences that hybridize to (a), under moderately stringent conditions; (e) sequences having at least 75% or 90% identity to (a); or (f) degenerate variants of (a). Polypeptides (ABP66596-1) and aptient and compositions comprising polypeptides (ABP66596 in a patient and compositions comprising polypeptides, polymolecities, artibodies, fusion proteins, T cell populations and antigen presenting cells expressing the polypeptide are useful in treating pancreatic cancer and simulating an immune response. The polymolecities can be used as probes or primers for nucleic acid hybridisation, in the design and probes or primers for nucleic acid hybridisation, in the design and proteins in the tumour cells, in vaccines and for gene therapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from NIPO at ftp.wipo.int/pub/published_pot_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDSSPVSSTVPAP 120
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Pred. No. 9.7e-65;
0; Mismatches 1,
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central/peripheral nervous system (NS). The method involves administering NS-specific antigen, its analogue or its central/peripheral nervous system (NS). The method involves administering NS-specific antigen, its analogue or its peptide, a nucleotide sequence the NS-specific antigen, its analogue or its combinations. The method is useful for promoting nerve regeneration and preventing neuronal degeneration in central/peripheral nervous system from injury/disease, where the injury is spinal cord injury, blunt camma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or autoimmune disease or neoplasm. The disease results in a degenerative canned and in either gray or white matter or both. The disease is not an autoimmune disease or neoplasm. The disease results in a degenerative concess occurring in either gray or white matter or both. The disease is disease, is claim to a concept by, senile dementia, Alzheimer a disease, parkinson's claese, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea, anyotrophic lateral sclerosis, non-arteritic optic neuropathy, and vitamine deficiency, intervertebral dise, hernistion, prion diseases such as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral concepty relain, hypoglycemia, Sjosyen blasson syndrome, acute sensory neuropathy, chronic ataxic neuropathy, billary cirrhosis, primary anyloidosis, obstructive lung diseases, acromegaly, malabsorption consolications of various diseases, including but not limited consory neuropathy, chronic ataxic neuropathy, billary cirrhosis, pathies, complications of various durgs (e.g., metronidazole) and toxins (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia, edisease, or lipoproteinemia. The present sequence represents the human consorransmitter receptor protein Nogo-B, an example of NS-specific

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US2002072493-A1 Homo sapiens

13-JUN-2002

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This invention describes novel nucleic acid molecules that are associated with apoptosis and encode a polypeptide and are derived from a normalised gene library (embryonic or liver) or cone collections, and the extent of apoptosis measured by cell death detection assay or the CPRG assay (measuring loss of membrane integrity). The products of the invention have extostatic, neuroprotective, immunosuppressive, antitheumatic, on antiarthritic, dermatological, antiinflammatory, hepatotropic, virucide, notropic, anticonvulsant, antiparkinsonian, vasotropic, crebroprotective and antialcoholic activity and can be used for gene therapy. The polynucleotides also related vectors, hosts (or their certacts), encoded polypeptide (or their receptors) and/or agents that inhibit their activity (including antisense sequences) are used for treatment or prevention of tumours, autoimmune or despenarative diseases and viral infections, specifically leukaemia, carcinoma, sarcoma, multiple sclerosis, rheumatoid arthritis, diabetes, lupus, or infection
SSGSVVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG 240
                                                                         288
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                                                                                                                                                                                                                                             nucleic acids involved in apoptosis, useful for diagnosis and itement of e.g. tumors and degenerative disease, also related proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antirheumatic; antiarthritic; dermatclogical; antiinflammatory; hepatotropic; virucide; nootropic; anticonvulsant; antiparkinsonian; vasotropic; cerebroprotective; antialcoholic; gene therapy; tumour; autoimmune disease; degenerative disease; viral infection; leukaemia; carcinoma; sarcoma; multiple solerosis; rheumatoid arthritis; diabetes; lupus; hepatitis; influenza viruses; Alzheimer's disease; Huntington's disease; Parkinson's disease; reperfusion injury; stroke;
                                                                                                      241 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            apoptosis; cell death; cytostatic; neuroprotective; immunosuppressive;
                                                                         VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSL
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with hepatitis or influenza viruses, Alzheimer's, Huntington's or
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                                                                                                                                                                                                                                                                                                                                                                                                    treatment of e.g. tumors a antibodies and modulators.
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Parkinson's diseases, reperfusion injury, stroke and alcoholic liver disease. Detection of the polymelectides and derived polypeptides can also be used for diagnosis of these diseases. This sequence represents an apoptosis-associated protein described in the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neuroprotective; gene therapy; BACE1 activity; RTN4; RTN3; amyloidosis;
Alzheimer's disease.
                                                                                                                                                              241 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSL
                                                                                                                                                                                                     AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP
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                                                                                                                                                1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEDEDEDLEELEVLERKPA
                                                                                                                                                                                                                                                                                                           174 -----VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG
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                                                                                                                        Gaps
                                                                                                                     12;
                                                                                          99.1%; Score 1833.8; DB 7; Length 373; 96.5%; Pred. No. 9.7e-65; ive 0; Mismatches 1; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 52; SEQ ID NO 8; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADK67503 standard; protein; 373 AA.
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                                                                                                                    Matches 360; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human RTN-4B protein.
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                                                                                                         Similarity
                                                                  Sequence 373 AA;
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                                                                                                                                                                                                                                        181 SSGSVVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG 240
                                                                                                                                                                                                                                                                VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSL 288
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                                                                                                                                                                                                                                                                                                     KFAVLMWVFTYVGALFNGLTLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK 348
                                                                                                                                                                                                                                                                                                             301 KFAVLMMVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK 360
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       The invention relates to an isolated polypeptide having BACE1 activity. The protein is RTM4 or RTM3 protein. The polypeptide is useful in preparing a composition for treating amyloidosis or Alzheimer's disease. This sequence corresponds to the RTM-4B protein.
                                                                                                                                                                                                                            -----WDLLYWRDIKKTGWVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKG
                                                                                                             1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEDEDEDLEELEVLERKPA
                                                                                                                        contactin-associated protein-1; Caspr; neuroprotective; gene therapy; CNS; spinal cord injury; multiple sclerosis; epilepsy; stroke.
                                                                                            Gaps
                                                                                            12;
                                                                         DB 7; Length 373;
                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human; Nogo-B; neurite outgrowth inhibitor; Nogo;
                                                                        Score 1833.8; DB 7
Pred. No. 9.7e-65;
0; Mismatches 1;
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                                                                        99.1%;
96.5%;
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20-JUN-2003; 2003US-0480138P
                                                                                                                                                                                                                                                                                                                                                                                                          standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                           Matches 360; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Nogo-B protein.
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                                                                                  Similarity
                                                       Sequence 373 AA;
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New composition comprising Nogo and Caspr or a substance capable of promoting interaction between Nogo and Caspr useful for treating injury to or disease of the CNS, e.g., spinal cord injury, multiple sclerosis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.1%; Score 1833.8; DB (96.5%; Pred. No. 9.7e-65; iive 0; Mismatches 1.
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/note= "NogoB (ASY) peptide"
                                                                                                                                                                               Disclosure; Page 14; 202pp; English.
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                                                                                                                epilepsy or stroke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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301 KFAVLMMVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neuroendocrine specific protein. The MAGI protein can be expressed by standard recombinant methodology. The MAGI polypeptides, polynucleotides and antibodies are useful for treating diseases, including neuropathies, spinal injury, neuronal degeneration, neuromuscular disorders, psychiatric disorders and developmental disorders, cancer, stroke and inflammantory disorders. The polynucleoitde is also useful for chromosome localization and for tissue expression studies. The present sequence represents the human MAGI protein
                              241 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSL
                                                                                                 KFAVLAWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MEDLIDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEEBEDEDLEELEVLERKPA
  229 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAGI protein; neuroendocrine-specific protein; neuropathy; human; spinal injury; neuronal degeneration; neuromuscular disorder; cancer; psychiatric disorder; developmental disorder; inflammatory disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEDEDLEELEVLERKPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel polypeptides related to neuroendocrine-specific proteins and polynuclectides useful for diagnosis of various diseases and for treatment of cancer and neurological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to human MAGI protein, which is similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3; Length 1192;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 stroke; cytostatic; cerebroprotective; neuroprotective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95.0%; Score 1756.9; DB 3; 30.3%; Pred. No. 8.5e-61; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                         AAY56967 standard; protein; 1192 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Page 20-21; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SMIK ) SMITHKLINE BEECHAM PLC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Michalovich D, Prinjha RK;
                                                                                                                                                                                                IQAKIPGLKRKAE 361
                                                                                                                                                                                                                                    361 IQAKIPGLKRKAE 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human MAGI polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-182693/16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAZ56886
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                                                                                                 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to a new method of identifying modulators of Nogo function or BACE activity. The method involves providing Nogo and BACE bylypetides capable of binding with each other, monitoring the interaction between these polypeptides, and determining if the test agent interaction between these polypeptides, and determining if the test agent caute neuronal injuries, such as spinal or head injury, stroke, peripheral nerve damage, and in neoplastic (e.g. glioblastomas, carriospinas), hyperproliferative or dysproliferative disorders (e.g. cirrhosis, peripheral nerve damage, and in neoplastic (e.g. glioblastomas, tissue cirrhosis, psoriasis, keloid formation, fibrocystic conditions, tissue hypertrophy) of the central nervous system. The BACE polypeptide is useful in screening methods to identify agents that may act as modulators of BACE activity and in particular agents that may act as modulators of nogo-associated diseases articular agents that may be useful in creating conditions the polynucleotide encoding the BACE polypeptide are useful in cresponsive to the modulation of Nogo activity, in alleviating the symptoms or improving the condition of a patient suffering from this disorder; in axon regeneration, or in preventing metastasis or spreading of a cancer. The polynucleotide may also be an essential component in creching the present amino acid sequence represents the human NogoB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying modulators of Nogo or BACE activity for treating acute neuronal injuries, neoplastic or dysproliferative disorders, comprises providing and monitoring interaction between Nogo and BACE polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPCWDPSPVSTVPAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEDEDLEELEVLERKPA
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          /note= "NogoB (ASY) peptide, distinguishes NogoB from other Nogo isoforms" 272. .285
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Pred. No. 2e-64;
1; Mismatches 2; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                    Prinjha R, Rowley A;
                                                                                              /note= "NogoB (ASY) peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 25; 68pp; English.
                                                                                                                                                                                                                                                                                                                                             (GLAX ) GLAXO GROUP LTD.
(SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                18-JAN-2002; 2002WO-GB000228.
                                                                                                                                                                                                                                                                                              18-JAN-2001; 2001GB-00001312.
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96.0%;
180. 193
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12 SPIGAMANGSELEDDREPRESSANGENERAL	Db 1141 LILALISLFSVFVIYERHQAQIDHYLGLANKNVKDAWAKIQAKIPGLKRKAE 1192	RESULT 13 AAB82349 ID AAB82349 standard; protein; 1192 AA.	AA AAB82349;	XX DT 23-JUL-2001 (first entry)	DE Human NOGO-A protein.	XA NOGO-A; human; chromosome 2p21; neuropathy; spinal injury; brain injury; XW ctroke, neuronal decemenation, altheimer's disease. Partinson's disease.			OS Homo sapiens.	AX AV200136631-A1.	AA PD 25-MAY-2001.	AA PF 14-NOV-2000; 2000WO-GB004345.	PR 15-NOV-1999; 99GB-00026995.	(2007-NED-17	_ ^	michalovich D, Fiinjua	N-PSI	New p	yene and may be userul in the treatment of medial disolution Alzheimer's and Parkinson's diseases.	PS Disclosure; Page 26-27; 25pp; English.				CC treatment of diseases including neuropathies, spinal injury, brain CC injury, stroke, neuronal deqeneration, for example Alzheimer's disease				SQ Sequence 1192 AA;	atch 95.0%; Score 1756.9; DB 4; Length 1192; cal Similarity 30.3%; Pred, No. 8.5e-61; Tanal 2011 Cont	Matches 361; Conservative 0; Mismatches 0; indels 831; Gaps 1;	Qy 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEEEEEEEEEELEVLERKPA 60 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEEEEEEEEEEELEVLERKPA 60	Qy 61 AGLSAAPVPTAPAAGAPLMDFQNDFVPPARRGPLPAAPVAPERQPSWDPSPVSSTVPAP 120 Db 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPARRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120	Qy 121 SPLSAAAVSPSKLPEDDEPPARPPPPASVSPQAEPVWTPPAPAAPPS 171
6 4 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8		121 SPLSAAAVSPSKLPEDDEPPARPPPPASVSPQAEPVWTPPAPAPAPPS	172	181 SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP	172	241 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	172;	301 GSSFSVSPKAESAVIVANPREBIIVKNKDEEEKLVSNNILHNQQELPTALTKLVKEDEVV	172	361 SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	172	421 DKKCFADSLEQTNHEKDSESSNDDTSPPSTPEGIKDRPGAYITCAPFNPAATESIATNIF	172	481 PLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTE	172	541 EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	172	601 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYE	172	661 EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE	172	721 MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMLVKESLTETSFESMI	172	781 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	172	841 SNDDLFISKEAQIRETETFSDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI	172	901 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSALAT	172TSUVDLLYWRDIKKTGVV	961 QAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLLYMRDIKKTGVV	190 FGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESE 	250 VAISEELVOKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTL 	

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SPLSAAAVSPSKLPEDDEPPARPPPPASVSPQAEPVWTPPAAPAPPSTPAAPKRRG 180
                                                                                                       241 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 300
                                                                                                                                                           301 GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHNQQELPTALTKLVKEDEVV 360
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                                                                                                                                                                                                              361 SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV 420
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                                                                                                                                                                                                                                                                   421 DKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIATNIF 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           961 QAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGVV
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                                                    SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFFSVLLETAASLPSLSP
                                                                                                                                                                                                                                                                                                                      481 PLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTE
                                                                                                                                                                                                                                                                                                                                                                         EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF
                                                                                                                                                                                                                                                                                                                                                                                                                              601 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      721 MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMLVKESLTETSFESMI
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cranial trauma; cerebral trauma; spinal cord injury; stroke; demyelination; demyelinating disease; multiple sclerosis; monophasis demyelination; encephalomyelitis; multifocal leukcencephalopathy; panencephalitis; Marchiafava-Bignami disease; pontine myelinolysis; adrenoleukodystrophy; Pelizacus-Merzbacher disease; Spongy degeneration; Alexander's disease; Canavan's disease; metachromatic leukodystrophy; viral infection; Krabbe's disease.
                                                                           nogo protein;
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/note= "This sequence is specīfically claimed"
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7/abel= Pepl
Anote= "Receptor binding inhibitory peptide.
sequence is specifically claimed"
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sequence is specifically claimed"
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[label= Pep4
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                                                                            antibody;
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claimed"
                                                                            growth; immunogen;
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AAU04591 standard; protein; 1192
                                                                            Nogo receptor; axonal
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/label= Pep2
                                     (first
                                                        Human Nogo protein.
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                                                                                                                                                                 Homo sapiens
                                    26-SEP-2001
                  AAU04591;
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2001-442138/47. (UYYA) UNIV YALE Strittmatter SM;

26-MAY-2000; 2000US-0207366P. 29-SEP-2000; 2000US-0236378P.

2000US-0175707P

12-JAN-2000;

12-JAN-2001; 2001WO-US001041

19-JUL-2001

Novel Nogo receptor protein useful for identifying modulator of Nogo protein or Nogo receptor protein, which is useful for treating central nervous system disorders. N-PSDB; AAS09453

Example 1; Page 101-104; 109pp; English.

The sequence is the human Nogo protein, a 250kDa myelin-associated axon growth inhibitor. The invention relates to the use of the nogo receptor, nogo protein, their nucleic acids, vectors expressing them and antibodies against them, to isolate agents which block nogo receptor mediated axonal growth. The agent is useful for treating a central nervous system disorder which is a result of cranial or cerebral trauma, spinal cord

actions of the organization disease actions of the multipolar intermediation manephalogous it is multipolar actions as endocasis, section and keepen action in the mysting basencephalics, waternolaukodystrophy, Pelitasua-Netzbaher disease, Spongy degeneration, Alexander's disease, Canavar's disease, Canavar's disease, Spongy degeneration, Alexander's disease, Canavar's dis	SEI SEI	172 901 172 961	1021	1081	Oy 310 LITALISLESVPVIYERHOAQIDHYLGLAN 	RESULT 15 ABG30938 ID ABG30938 standard; protein; 1192 AA.	XX AC ABG30938;	DT 21-OCT-2002 (first entry)	DE Human NogoA protein.		KW tissue hypertrophy; central nervous sys KW Noo-associated disease; metastasis.		XX XX WOODSEARS			18-JAN-2001;	GROUP LID.	ALMS)	WPI; 2002-599722/64.		PT identifying modulators of Nogo or BACE PT neuronal injuries, neoplastic or dyspro			CC The present invention relates to a new CC of Nogo function or BACE activity. The CC BACE nothing with the CC BACE noth				
	8 4 8 4 8 4 8 4 8 4 8 4 8 4 8 4 8 4 8 4	injury, stroke or a demyelinating disease selected from multiple sclerosis, monophasis demyelination, encephalomyelitis, multifocal leukoencephalopathy, panencephalitis, Marchiafava-Bignami disease, pontine myelinolysis, adrenoleukodystrophy, Pelizaeus Merzbacher dis Spongy degeneration, Alexander's disease, Canavan's disease, metachromatic leukodystrophy, viral infection and Krabbe's disease Sequence 1192 AA;	95.0%; Score 1756.9; DB 4; Length 1192; imilarity 30.3%; Pred. No. 8.5e-61; Conservative 0; Mismatches 0; Indels 831; Gaps	1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEDEDEDLEELEVLERKFPA 	61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAFERQPSWDPSPVSSTVPAP 	121 SPLSAAAVSPSKLPEDDEPPARPPPPPASVSPQAEPVWTPPAPAPAPPS	2	181 SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP		241 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	301 GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHNQQELPTALTKLVKEDEVV	172	361 SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	2	421 DKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	2	481 PLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPPLVAAQDSETDXVTTDNLTKVTE	1/2	172	601 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPYE	2	661 EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE	172	721 MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMLVKESLTETSFESMI	172	781 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	172	841 SNDDLFISKEAQIRETETFSDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI

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GFLVDDLVDSLKFAVLMWVFTYVGALFNGLTL 309
                                                                                                                                                                                                  SVTISFRIYKGVIQAIQKSDEGHPFRAYLESE 249
                                                                                                      DRSPSAIFSAELSKTSVVDLLYWRDIKKTGVV 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a new method of identifying modulators of Nogo function or BACE activity. The method involves providing Nogo and BACE polypeptides capable of binding with each other, monitoring the interaction between these polypeptides, and determining if the test agent is a modulator of Nogo or BACE activity. The method is useful in treating acute neuronal injuries, such as spinal or head injury, stroke, peripheral nerve damage, and in neoplastic (e.g. glioblastomas, neuroblastomas), hyperproliferative or dysproliferative disorders (e.g. cirrhosis, psoriasis, keloid formation, fibrocystic conditions, tissue hypertrophy) of the central nervous system. The BACE polypeptide is useful in screening methods to identify agents that may act as modulators
                                                                   -----TSVVDLLYWRDIKKTGVV 189
SEKISFSDDFSKNGSATSKVLLLPPDVSALAT 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B activity for treating acute roliferative disorders, comprises between Nogo and BACB polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ury; spinal injury; head injury;
lastic disorder; glioblastoma;
order; dysproliferative disorder;
n; fibrocystic condition; cancer;
ystem; axon regeneration; NogoA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rowley A;
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of BACE activity and in particular agents that may be useful in treating Nogo-associated diseases. The modulators of Nogo or BACE polypeptides, and the polynucleotide encoding the BACE polypeptide are useful in manufacturing a medicament for the treatment or prevention of disorders symptoms or improving the condition of a patient suffering from this disorder, in axon regeneration, or in preventing metastasis or spreading of a cancer. The polynucleotide may also be an essential component in assays, a probe, in recombinant protein synthesis, and in gene therapy techniques. The present amino acid sequence represents the human NogoA protein of the invention

Sequence 1192 AA;

9 1 MEDLDÓSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEDEDEDLEELEVLERKPA Gaps 95.0%; 30.3%; Matches 361; Conservative Local Similarity Query Match ઠ ΩD

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171 172

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301 GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHNQQELPTALTKLVKEDEVV 360 ---- 171 SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV 420

172

171 540

PLLGDPTSENKTDEKKI EEKKAQI VTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTE

481

661 EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE 720

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171

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961 QAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLYWRDIKKTGVV 1020 1081 VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMMVFTYVGALFNGLTL 1140 1021 FGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESE 1080 249 171 900 171 901 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSALAT 960 841 SNDDLFISKEAQIRETETFSDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESE VAISEBLVQKYSNSALGHVNCTIKELRRIFLVDDLVDSLKFAVLMWVFTYVGALFNGLTL 1141 LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1192 310 LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 361 . 052 172 172 172 190 ò 셤 ઠે g 8 8 ò g 유 8

Search completed: June 23, 2005, 10:52:04 Job time : 118.158 secs

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Thu Jun 23 10:59:56 2005
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GenCore VerBlon 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd. OM protein - protein search, using sw model Run on: June 23, 2005, 10:29:31 ; Search time 25.0347 Seconds (without alignments) 1387.446 Million cell updates/sec	1387.446 Million cell updates/sec
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US-09-830-972-29-FUSED 1850 1 MEDLDQSPLVSSSDSPPRPQ......VKDAMAKIQAKIPGLKRKAE 361 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.1 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES		
Result	Score	Query	Query Match Length	DB	TD CT	Description	
				1			
п	827.7	44.7	116	7	A46583	neuroendocrine-spe	
8	684.2	37.0	208	7	I60904	neuroendocrine-spe	
e	999	36.0	267	7	A60021	tropomyosin-relate	
4	454.3	24.6	2484	~	T26216	hypothetical prote	
S	447	24.2	. 2607	0	T26215	hypothetical prote	
9	353.5	19.1	222	7	T26213		
7	275.1	14.9	1173	~	T31421	C-terminal domain-	
80	266	14.4	1206	7	S24407	formin isoform IV	
6	266	14.4	1468	~	811515	formin - mouse	
10	264.1	14.3	1058	N	T13286	cappuccino gene pr	
11	262.4	14.2	1611	7	T38236	hypothetical prote	
12	260.9	14.1		7	F86387	probable Pto kinas	
13	257.1	13.9		0	A59295 ·	unconventional myo	
14	256.5	13.9		0	T31065	diaphanous protein	
15	255.5	13.8		0	A59266	unconventional myo	
16	253.8	13.7		8	A35098	MHC class III hist	
17	253.6	13.7		~	G86441	unknown protein [i	
18	250.9	13.6	-	7	JC8033	leukocyte formin p	
19	250.4	13.5		7	D89756	protein T23E7.2b [
20	250	13.5		7	S54986	regulatory protein	
21	247.7	13.4	_	0	JC6552	DNA topoisomerase	
22	247.5	13.4		7	B86369	hypothetical prote	
23	247.3	13.4	980	7	G75523	probable cellidivi	
24	247.2	13.4		7	A55617	masquerade precurs	
25	247	13.4	2090		S26058	probable transform	
26	244.8	13.2	1127	7	T32404	hypothetical prote	
27	244.8		1375	7	S48375	hypothetical prote	
28	243.6	13.2	1721	7	138902	retinoblastoma bin	
29	243.4	13.2	3938	~	T42761	Bassoon protein -	_
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					•		

hypothetical prote	progesterone recep	hypothetical prote	hypothetical prote	hypothetical prote	progesterone recep	proline-rich prote	progesterone recep	zinc finger protei	BPLF1 protein - hu	T20H2.9 protein -	hypothetical prote	hypothetical prote	neurofilament trip	BNI1 protein - yea	proline-rich prote
D96711	A35466	E96636	T26517	T26998	QRHUP	S16748	A25923	I84499	QOBE8	A86335	D96728	T51023	T49592	S63244	S21961
7	~	0	~	~	ч	0	7	0	-	~	~	~	~	~	0
708 2	786 2	907 2	1634 2	716 2	933 1	449 2	930 2	1706 2	3149 1	1137 2	710 2	2649 2	765 2	1953 2	534 2
	13.2 786 2														
13.2		13.1	13.1	13.1	13.1	12.9	12.9	12.9	12.9	12.8	12.8	12.8	12.7	12.7	12.7

ALIGNMENTS

HARINOUNDA A A A A A A A A A A A A A A A A A A	RESULT 1 A46583 Nucroendocrine-specific protein, splice form A - human NiContains: neuroendocrine-specific protein, splice form B C;5pecies: Homo sapiens (man) C;5pecies: Homo sapiens (man) C;5pecies: Homo sapiens (man) C;5pecies: Homo sapiens (man) C;5pecies: Homo sapiens (man) C;5pecies: Homo sapiens (man) C;5pecies: Homo sapiens (man) C;5pecies: Homo sapiens (man) C;5pecies: Homo sapiens (man) C;5pecies: Homo sapiens (man) C;5pecies: Homo sapiens (man) C;5pecies: Homo sapiens Requested: Cloima and expression of alternative transcripts of a novel neuroendocrine-spec A;7tles: Cloima and expression of alternative transcripts of a novel neuroendocrine-spec A;7tles: Cloima and expression of alternative transcripts of a novel neuroendocrine-spec A;7tles: Cloima and expression of alternative transcripts of a novel neuroendocrine-spec A;7tles: Cloima ary, translated from GB/EMBL/DDBJ A;6cession: Logolo A;6cession: Logolo A;6cession: Logolo A;6cession: Logolo A;6cession: RNA A;6ces	Ramaekers, F.C.; Vē neuroendocrine-spec 1950.1; PID:g307307
	A;Gėne: GDB:RTN1; NSP A;Cross-references: GDB:203968; OMIM:600865 A;Map position: 14q21-14q22	
	Query Match 44.7%; Score 827.7; DB 2; Length 776; Best Local Similarity 27.1%; Pred. No. 4.8e-20; Matches 196; Conservative 55; Mismatches 89; Indels 383; Gaps	17;
ò	6 QSPL	
qa	70 GSPVAMETASTGVAGVSSAMDHTFSTTSKDGEGSCYTSLISDICYPPQEDSTYFTGILQK 129	29
λο qa	10VSSSDSPPRPQP	21 189
λ _o dd	22AFKYQFVREPEDEBEBEBEBEDEDELE	50 249
<i>장</i> 점	S1	53 309
<u>ک</u> ک	54VLERKPAAGLS	64 369
λό ———	65AAPV	78

tropomyosin-related protein, neuronal - rat C;Species: Rattus norvegicus (Norway rat) C;Species: Rattus norvegicus (Norway rat) C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 05-Nov-1999 C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 05-Nov-1999 C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 05-Nov-1999 C;Date: 03-Mar-1993 #sequence_revision Res. 10, 33-41, 1991 A;Fitle: Developmentally regulated cDNA expressed exclusively in neural tissue. A;Reference number: A60021; MUD:91278684; PMID:1647480 A;Residues: A60021 A;Molecule type: mRNA A;Residues: 1-267 **WIES A;Cross-references: EMBL:X52817; NID:9456549; PIDN:CAA37001.1; PID:9456550 C;Comment: This neuronal-specific mRNA was identified by hybridization to an alpha-tropon	Query Match 36.0%; Score 666; DB 2; Length 267; Best Local Similarity 66.1%; Pred. No. 1e-15; Matches 123; Conservative 34; Mismatches 29; Indels 0; Gaps 0; Qy 172 TSVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQ 231 : :	Qy 232 AIOKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFA 291 Db 70 AVQKTDEGHPFRAYLELEITLESQEQIQKYTDCLQLYVNSTLKELRRLFLVQDLVDSLKFA 129 Qy 292 VLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKVVKDAMAKIQA 351 Db 130 VLMWLLTYVGALFNGLTLLILALISLFSVPVYYKHQAQYDQYLGLVRTHINTVVAKIQA 189	Qy 352 KIPGIK 357 Db 190 KIPGIK 357 Db 190 KIPGIR 195 Db 190 KIPGIR 195 FESULT 4 T26216 T26216 T30 Gamonthabditis elegans C.Decise: Camonthabditis elegans C.Decise: Camonthabditis elegans C.Decise: T15-Oct-1999 #text_change 09-Jul-2004 C.Decision: T26216 T30-10 Shandited to the PMBL Data Library, August 1996 A.Accession: T26216 A.Accession: T26216 A.Accession: T26217 A.Accession: T26216 A.Accessio
370 TAENPRPVGQLADRPEVKARSGPPTIPSPLDHEASSAESGDSEIELVSEDPMAAEDA 79MDFGNDFVPPAPRGPLPAAPPV	594 239 654	Qy 299 YVGALENGLTLILALISLFSVPVIYERHQAQIDHYLGLANROVVDAMAKIQAKIPGLKR 358 Db	RESULT 2 160904 neuroendocrine-specific protein C - human C; Species: Home saptems (man) C; Home saptems (man) C; Home saptems (man) C; Home saptems (man)

S. S. S. S. S. S.

A;Cross-references: UNIPROT:Q23188; EMBL:Z78066; PIDN:CAB01523.1; GSPDB:GN00023; CESP:Wd A;Experimental source: clone W06A7 C;Genetics: A;Gene: CESP:W06A7.3b A:Map Dosition: 5	
Introns: 27/1; 77/2; 201/2	ληρορώς επικορούς και ο που και ο που ο πο
Query Match 19.1%; Score 353.5; DB 2; Length 222; Best Local Similarity 32.2%; Pred. No. 2.6e-05; Matches 65; Conservative 48; Mismatches 84; Indels 5; Gaps 1;	116TVPAPSPLS
QY 156 BPVWTPPAPAPPSTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALA 215	DO 532 ERKSGDLERLFARVERSGRUKUSKRKGAVFFSLQULIDHDLFALKRIIIVGKFURIEFKA 591 Qy 125AAAVSPS 131
Qy 216 LLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKEL 275	Db 592 PSPAPAVSPKGEVLYDSEGLSADERGAKGDKDRRRRSGAASSSSSREKASRRKALDGDRG 651 Qy 132KLPEDDEP
276 RRLFLVDDLVDSLKPAVLMMVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYL	Db 652 RDRDRSSKKPRTPKDSAPGSGALPKAPPRSGSSSSSSSSSRKVKLQSKVAVLIREGVSS 711 Qy 140 139
DD 129 KKLVFVESPLESIKFGLVLWSLTYIASWFSGFTLAILGLLGVFSVPKVYESNQEAIDPHL 188 Qy 336 GLANKNVKDAMAKIQAKIPGLK 357 : :: : :	Db 712 TTPAKDSSSSGLGSIGVKFSRDRESRSPFLKPDERSPAEGVKVAPGSTKPKKTKAKAKAG 771
Db 189 ATISGHLKAVQNIİDEKLPFLR 210	772 AKKAKGTKGKTKPSKTRKKVRSGGSSTASGGPGSLKKSKADSCSQAASAKGTEETSWSGE
Figure 1 domain-binding protein rA1 - rat Species: Rattus norvegicus (Norway rat) Bate: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004 Maccassion: 731421 Maccassion: 731421 Maccassion: 731421 The C-terminal domain of the largest subunit of RNA polymerase II Reference number: Z21024; MUID: 96293459; PMID: 8692929 Molecule type: mRNA; Molecule type: mRNA; Molecule type: MRNA; Molecule	0y 140PARPPP
DD	Ridackson-Chrubby, L.; Kuo, A.; Leder, F. Genes Dev. 6, 29-37, 1992 A;Title: A variant limb deformity transcript expressed in the embryonic mouse limb define A;Reference number: \$24407; MUID:92112033; PMID:1339380 A;Accession: \$24407 A;Accession: \$2407

A;Residues: 1-1206 <jac> A;Cross-references: UNIPROT:Q05859; EMBL:X62379; NID:g51552; PIDN:CAA44244.1; PID:g51553</jac>	737 EEIETLQAQFELKTFHIRGEHALVTARLEEAIENLKQQLEKRREGCEEMRDVCISTDDDC
Query Match 14.4%; Score 266; DB 2; Length 1206; Best Local Similarity 17.3%; Pred. No. 1.7; Matches 102; Conservative 40; Mismatches 97; Indels 350; Gaps 24;	59 -PAA
Oy 5 DQSPLVSSSDSPPRPQPAFKYQFVRBPEDEEBEEEEE 41	Qy 62 -GLSAAEVPTAFAAGAFUMDFGNDFVPFAPRGFLPAAPFVAPERQ 105 D
42 EEDE	OY 106 PSWDPSPVSSTVPAPSPLSAAAVSPSKLPEDDEPPARPPPPPARSVSPQAEP 157
- PAA	Qy 158 VWTPPAPAPAAPSTSVVDLLYWRDIKKTGVVFGASLF 195
62 -GLSAAPVPTAPAGAPLMDFGNDFVDPAPGPLPAAPVAPERO	LSVTISFRIYKGVIQAIQKSDEGHPFRAY
CY 106 PSWDPSPVSSTVPAPSPLSAAAVSPSKLPEDDEPPARPPPPPASVSPQAEP 157	Qy 246 LESEVAISEELVQ
OY 158 VWTPPAPAPAAPPSTSVVDLLYWRDIKKTGVVFGASLF 195 	Qy 278 -LFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLG 336
Qy 196 LLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAY 245 Db 777	Qy 337 LANKAVKDAMAKIQAKIPGLKRKAE 361
CY 246 LESBVAISEELVQ	RESULT 10 T13286 cappuccino gene protein - fruit fly (Drosophila melanogaster)
Qy 278 -LFLVDDLVDSLKFAVLMMVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLG 336 	C;Species: Drosophila melanogaster C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004 C;Accession: T13286 R;Emmons, S.; Phan, H.; Calley, J.; Chen, W.; James, B.; Manseau, L.
337 LANKNVKDAMAKIQ	Genes Dev. 9, 2482-2494, 1995 A;Title: Cappuccino, a Drosophila maternal effect rene required for polarity of the egg & A;Reference number: 217651; MUID:96033799; PMID:7590229 A;Reference number: Langland from CB/DMB1/DNB1
RESULT 9 \$11515 formin - mouse C,Species: Mus musculus (house mouse) C;Date: 22-Jan-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004	A; Modecule type: mRNA A; Residues: 1-1058 <emm> A; Residues: 1-1058 <emm> A; Cross-references: UNIPROT: Q24120; EMBL: U34258; NID: g1061333; PID: g1061334; PIDN: AAC469; C; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Cross-references: PlyBase: FBgn0000256</emm></emm>
Vogt, T.F.	Query Match Best Local Similarity 16.1%; Pred. No. 1.4; Matches 118; Conservative 47; Mismatches 117; Indels 449; Gaps 27;
A; Reference number: S11515; MUID: 90363291; PMID: 2392150 A; Accession: S11515 A; Molecule type: mRNA A; Reddues: 1-1468 < MOY> A; Cross-references: UNIPROT: Q05860; EMBL: X53599; NID: 952877; PIDN: CAA37668.1; PID: 952878	Qy 9 LVSSSDSPPR
66; DB 2; Length 1468; 0. 2.8; atches 97; Indels 350; Gaps 24	43EDEDEDLEELEVLERKPAAGLSAAPVPTAPAAGAPLMDFGNDFV-PP
Qy 5 DQSPLVSSSDSPPRPQPAPKYQFVREPEDEEE	89 APRGPLPAAPPVAPERQPSWDPSPVSSTVPAPSPLSAAAVSPSKLPEDDEPPAR 502 PPPPPPPPPPPLANYGAPPPPPPPPPPGSGSAPPPPPPAFIEGGGG
bedl	Qy 143 -PPPPPPASVSPQAEPV

Qy 293 308 Db 554 KSSNIILENNEHALVSDPGLAKIALDCNTHITTFWMGTPGYMAPEYASGKLTFKSDVPS 613	Qy 309LLILALIS	RESULT 13 A59295 unconventional myosin-15 - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004 C;Accession: A59295 R;Liang, Y.; Wang, A.; Belyantseva, I.A.; Anderson, D.W.; Probst, F.J.; Barber, T.D.; Mil an, T.B.; Fridell, R.A. Genomics 61, 243-258, 1999 A;Title: Characterization of the human and mouse unconventional myosin XV genes responsil	A;Status: A55295 A;Status: preliminary; not compared with conceptual translation A;Status: preliminary; not compared with conceptual translation A;Status: mRNA A;Residues: 1-3511 <lia> A;Cross-references: UNIPROT:Q9QZZ4; GB:AF144095; NID:g6224684; PIDN:AAF05904.1; PID:g6224; G;Genetics: A;Genetics: A;Gene: MGI:Nyol5 A;Cross-references: MGI:1261811 A;Map position: 11:33.9 F;1209-1871/Domain: myosin motor domain homology <mmo></mmo></lia>	Query Match 13.9%; Score 257.1; DB 2; Length 3511; Best Local Similarity 9.5%; Pred. No. 50; Matches 136; Conservative 46; Mismatches 113; Indels 1139; Gaps 35; Qy 16 PPRPQPAFKYQFV	4 N	Db 549 GPEFGHPTPRATSLARFLKKTLSEKKPIPRLRGSQKARGGRPPVREAAYKRFGYKLAGM 608 Qy 102 -PER	Db 669 PPFSPTFSRPPRLASPYGSLRQHPPPWAAPAHVPFPPQANWWGFAEPPGTSPEVAPDLLA 728 Qy 130
Db 1499 INKQTFGGVIYKAVGNVTVQQIGEIRPGDIVTFDKAKFSGGK 1540	RESULT 12 P86387. probable Pto kinase interactor [imported] - Arabidopsis thaliana C;Deteis: Arabidopsis thaliana (mouse-ear cress) C;Deteis: Arabidopsis thaliana (mouse-ear cress) C;Deteis: Arabidopsis thaliana (mouse-ear cress) C;Deteis: D2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004 C;Accession: F86387 R;Theologis, A:, Ecker, J.R.; Palm, C.J.; Federapiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Cressy, T.H.; Dewar, K.; ansen, N.P.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C.C.A; Li, J.H.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, C.A.; Li, J.H.; Li, J.H.; Lin, X.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,	Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A, Authores: Salzberg, S.L.; Schwartz, J.Y.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A, Authores: Salzberg, S.L.; Schwartz, J.Y.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A,Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A,Reference number: A86141; MUID:21016719; PMID:11130712 A,Recession: R86387 A,Status: preliminary A,Molecule type: DNA A,Residues: 1-760 <sto> A,Cross-references: UNIPROT:09C660; GB:AE005172; NID:gl1079512; PIDN:AAG29223.1; GSPDB:GC;Genetics: A,Map position: 1</sto>	14.1%; Score 260.9; DB 2;		OY 141 ARPPPPPPASVSPQAEP	Qy 196 LLLSLTVFSIVSVTAYIALALLSV	Qy 224RIYKGVIQAIQKSDEGHPPRAYLESEVAISEELVQKYSNSALGHVNCT 271 Db

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QQ	789 QLSLRRGPFQPPFRPPPRRPQSLREAFSLRRASGRLGPPRSPVLGSPRPPSPPLLKHGP 848	R; Wata
ò	130PSKLPEDDEPPAR	A, Title
qq	849 RHRSLNLPSRLPRTWRRLSEPPTRAVKPWVHRAYPPPPSAGPWGASTGALEQQENQREAE 908	A, Rele
ζ	147Sysp 153 A	A; Molec
ΩP	909 DSETPWTVPPLAPSWDVDMPPTQRPPSPWPEGIGSLRGFSRPPPVPENPLLEHTSPSCEP 968 A	A; Cros
8	154 QAB 156	DOOR!!
qq	969 QSEDRVSNLTGIFLGQHHDPGPGQLTKSADPSLEKPEEVVTLGDPQPPAEPEALNPTPPN 1028	Best
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qq	1089 RAEPGRFAVVMPQVRGVSSFRPKGPAPVQPPEHPDQDPEQGPAPQACSLRWPCLWPPTDA 1148	Š 18
ò	171STSV 174	g ;
qq	1149 HCLWSRIRTYSSQSHLRGHGGDCHKSLWKKTRPQSWQNKMHSIRNLPSMRSREQHREDGV 1208	È d
δy	FLLESLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQ 234	8 8
qq	1209 EDMTQLEDLQETTVLANLKTRFERNLIYTYIGSILVSV 1246	<u> </u>
ò	235 KSDEGHPFRAYLESEVAISEELVQXYSNSALG	ą ;
qq	1247NPYRMFAIYGPEQVQQYSGRALGENPPHLFAIANLÀFAKMLDAKQNQCVII 1297	à á
ò	267 266	Q ;
qq	1298 SGESGSGKTEATKLILRCLAAMNQRRDVWQQIKILEATPLLEAFGNAKTVRNDNSSRFGK 1357	ें दे
ζó	267 268	ą ;
qq	1358 FVEIFLEGGVICGAITSQYLLEKSRIVFQAKNERNYHIFYELLAGLPAQLRQAFSLQEAE 1417	à á
δ	269 NCTI KELRRLF	ą ;
. qq	1418 TYYYLNQGGNCEIAGKSDADDFRRLLAAMEVLGFTSEDQDSIFRILASILHLGNVYFEKH 1477	à á
δ	280	3 8
qq	1478 ETDAQEVASVVSAREIQAVAELLQVSPEGLQKAITFKVTETIREKIFTPLTVESAVDARD 1537	i d
λ	284 LVDSLKFAVLM-WVFTXVGALFNGLTLILALI 315	3 8
qq	1538 AIAKVLYALLEGWLITRVNALVSPKQDTLSIAILDIYGFEDLSFNSFEQLCINYANENLO 1597	; f
ά	316 SLESUPUIYERHQAQ 330	3 ;
qq	1598 YLFN-KIVFQEEQEEYIREQMDWREIAFADNQPCINLISLKPYGILRILDDQCCFPQATD 1656	÷ 6
ά	331KDAM 346	; ;
QQ	1657 HTFLQKCHYHHGANPLYSKPKMPLPEFTIKHYAGKVTYQVHKFLDKNHDQVRQDVLFV 1716	<u> </u>
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Ор	1717 HSRIRVVAHLESSHAAQTAPPRLGKSSSITRLYKAHTVAAKFQQSLLDLVEKME 1770	<u>a</u>
		;

T31065
diaphanous protein homolog p140mDia - mouse
C;Species: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T31065

RESULT 14

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anabe, N.; Madaule, P.; Reid, T.; Ishizaki, T.; Watanabe, G.; Kakizuka, A.; Saito, J. J. 16, 3044-3056, 1997
J. 16, 2144-3056, 1997
J. 16, Pidyombia, a mammalian homolog of Drosophila diaphanous, is a target protein for erence number: Z20961; MUID:97357293; PMID:9214622
ession: T31065
                                                                                                                                         tus: preliminary; translated from GB/EMBL/DDBJ
ecule type: mRNA
idues: 1-1255 «WAT»
ses-references: UNIPROT:008808; EMBL:U96963; NID:g2114472; PID:g2114473; PIDN:AAC5328
e: binds to GTP-bound form of Rho and binds to profilin
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152 SPQAEDVWTP	Db 1696 LPBFTIKHYAGKVTYQVHKFLDKGHDQVRQDVLDLFVRSRTRVVAHLFSSHAPQAAPQRL 1755 Qy 347AXIQAKIPGLKBKAE 361 Db 1756 GKSSSVTRLYKAHTVAAKPQQSLLDLVBKAME 1786 Search completed: June 23, 2005, 10:57:02 Job time: 33.0347 secs
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Thu Jun 23 10:59:56 2005
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GenCore version 5.1.6
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OM protein - protein search, using sw model

June 23, 2005, 10:17:56; Search time 114.158 Seconds (without alignments) 1619.338 Million cell updates/sec Run on:

US-09-830-972-29-FUSED Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.1 Scoring table:

1612378 seqs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Description	Q96b16 homo sapien	Q9nqc3 homo sapien		-	Q8bh78 mus musculu	_	Q9jk11 rattus norv	Q8bgm9 mus musculu	Q8k3g8 mus musculu		Q8bgk7 mus musculu			Q6rss8 gallus gall		Q6im70 sus scrofa			Q6jrv2 xenopus lae	Q6jrv0 xenopus lae		Q99p72 mus musculu	Q6ify4 xenopus tro	xenobna	Q6jrv3 xenopus lae	xenobna	Q6jrv7 xenopus lae		gallus g	xenobna	Q6jrw0 xenopus lae
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	* Query Match	99.1	95.0	90.3	82.9	82.3	81.8	79.9	78.7	77.9	55.6	53.7	53.5	53.3	52.7	50.1	49.9	49.7	49.6	49.4	49.3	49.3	49.2	48.9	48.7	48.5	47.9	47.8	47.7	47.7	47.6	47.5
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O6jrw2 xenopus lae O99m33 macaca fasc O99m33 macaca fasc O8Wt00 mus musculu O16799 homo sapien Q8K484 mus musculu O64548 rattus norv O90638 gallus gall Q61fy5 xenopus lae O6jrw3 xenopu	,
QGURW2 QGGW33 QBKGTO QBKGTO QBKAĞ4 RTN1, HUMAN QBKAĞ4 RTN1, RAT QGGTRY5 QGGTRY5 QGGTRY4 QGGTRW4 QGGTRW4	
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316 1796 776 777 777 777 1993 1199	7
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873.1 867 829.8 829.8 827.7 825.8 818.1 793.3 779.7 779.7 779.7 751.7	3
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ALIGNMENTS

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SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3)
  300
                                                                                                                                                                              61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPARGPLPAAPPVAPERQPSWDFSPVSSTVPAP 120
                                                                                                                                                                                                                             SPLSAAAVSPSKLPEDDEPPARPPPPASVSPQAEPVWTPPAAPAPPST----- 172
                                                                                                                                                                                                                                       269
                                                                                                                                                                                                                                                                                                                                                               270 CTIKELRRIFLVDDLVDSLKFAVLMMVFTYVGALFNGLTLLILALISLFSVPVIYERHQA 329
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                                                                                                                                                        1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEEDEDLEELEVLERKPA
                                                                                                                                                                                                     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP
                                                                                                                                                                                                                                                                                                                    210 AYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVN
                                                                                                                                                                                                                                                                                                                                 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEEDEDEDLEELEVLERKPA
                                                                                                                Gaps
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MEDLINE=20129242; PubMed=10667780; DOI=10.1038/35000287;
Prinjha R., Moore S.E., Vinson M., Blake S., Morrow R., Christie G., Michalovich D., Simmons D.L., Walsh F.S.;
"Inhibitor of neurite outgrowth in humans.";
Nature 403:383-384(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE_21010696; PubMed=11126160; DOI=10.1038/sj.onc.1203948; Tagami S., Eguchi Y., Kinoshita M., Takeda M., Tsujimoto Y.; "A novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 on endoplasmic reticulum and reduces their anti-apoptotic activity."; Oncogene 19:5736-5746(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)
(Neuroendocrine-specific protein) (NSP) (Neuroendocrine specific protein C homolog) (RTN-x) (Reticulon 5) (My043 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                              31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RTN4_HUMAN STANDARD; PRT; 1192 AA.
Q9NQC3; O94962; Q9BXG5; Q9H212; Q9H313; Q9UQ42; Q9Y293; Q9Y2Y7;
                                                                                         DB 2; Length 392;
                                                                                                  Pred. No. 1.4e-51;
1; Mismatches 0; Indels
                                          Pfam; PF02453; Reticulon; 1.
PROSITE; PS50845; RETICULON; 1.
SEQUENCE 392 Aa; 42274 MW; D7B2AA5E839E58AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                       361 QIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 392
                                                                                                                                                                                                                                                                                                                                                                                                           330 QIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 361
EMBL; AX102278; AAM64247.1; -.
EMBL; AX102285; AAM64242.1; -.
GO; GO:0005783; C:endoplasmic reticulum; IEA.
InterPro; IPR003388; Reticulon.
                                                                                         Score 1833.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=RTN4; Synonyms=ASY, KIAA0886, NOGO;
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                                                                                         99.18;
                                                                                                    91.8%;
                                                                                                  Best Local Similarity 91.8
Matches 360; Conservative
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                                                                                                                                                                                                                                                                       173
                                                                                        Query Match
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Jin W.-L., Ju G., "Developmentally-regulated alternative splicing in a novel Nogo-A."; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=99156230; PubMed=10048485;
MEDLINE=99156230; PubMed=10048485;
Migage T., Ishikawa K.-I., Suyama M., Kikuno R., Hirosawa M.,
Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XII
The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro.";
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Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,
Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Song H., Peng Y., Zhou J., Huang Q., Dai M., Mao Y.M., Yu Y., Xu Luo B., Hu R., Chen J., "Human neuroendocrine-specific protein C (NSP) homolog gene."; Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y_{\rm u} J., Han L.H.; "Novel human cDNA clones with function of inhibiting cancer cell
MEDLINE=20237542; PubMed=10773680;
Yang J., Yu L., Bi A.D., Zhao S.-Y.;
"Assignment of the human reticulon 4 gene (RTN4) to chromosome
2p14-->2p13 by radiation hybrid mapping.";
Cytogenet. Cell Genet. 88:101-102(2000).
                                                                                                                                                                                                                                                                                                                                                                  "Cloning of a member of the reticulon gene family in human."; Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Isolation of a cell death-inducing gene.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                                  TISSUE-Placenta, and Skeletal muscle; Ito T., Schwartz S.M.;
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORMS 2 AND 3)
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                                   MEDLINE=20099367; PubMed=11042152; DOI=10.1101/gr.140200; Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G., Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G., Zhong M., Wu X.-R., Han Z.-G., Zhang J.-W., Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.; Cloning and functional analysis of cDNAs with open reading frames for stem/progenitor cells."; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M., Chen Z.; Gu G. M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                regeneration.";
J. Neurosci. Res. 67:559-565(2002).
J. Neurosci. Res. 67:559-565(2002).
J. Neurosci. Res. 67:559-565(2002).
Jock the regeneration of the nervous central system in adults.
Lisoform 2 reduces the anti-apoptotic activity of Bcl-x1 and Bcl-2.
This is likely consecutive to their change in subcellular location, from the mitochondria to the endoplasmic reticulum, after binding and sequestration.
-! SUBGUNIT: Binds to RTN4R. Interacts with Bcl-x1 and Bcl-2.
-! SUBCELIULAR LOCATION: Integral membrane protein. Endoplasmic reticulum reticulum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fournier A.E., Grandpre T., Strittmatter S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21888956; PubMed=11891768; DOI=10.1002/jnr.10134; Ng C.E.L., Tang B.L.; "Nogos and the Nogo-66 receptor: factors inhibiting CNS neuron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Contains 1 reticulon domain. CAUTION: Ref.11 sequence differs from that shown due to frameshifts in positions 1149 and 1156.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GrandPre T., Nakamura F., Vartanian T., Strittmatter S.M., "Identification of the Nogo inhibitor of axon regeneration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21069055; PubMed=11201742; DOI=10.1038/35053072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WEDLINE=20129259; PubMed=10667797; DOI=10.1038/35000226;
                                                                                                                                                                                                                                                                          Mao Y.M., Xie Y., Zheng Z.H.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                   Li J.M.;
to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       through 2 putative transmembrane domains.

LIERMATIVE PRODUCTS:

Event_Alternative splicing; Named isoforms=4;

Name=1, Synonyms=RTN 4A, Nogo-A, RTN-XL;

Isold=Q9NQC3-1; Sequence=Displayed;

Name=2; Synonyms=RTN 4B, Nogo-B, RTN-XS, Foocen-M;

Isold=Q9NQC3-2; Sequence=VSP 005655;

Name=3; Synonyms=RTN 4C, Nogo-C, Foocen-S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=09NQC3-3; Sequence=VSP_005652, VSP_005653;
                                                                                                                                                                                                                                    SEQUENCE OF 482-1192 FROM N.A. (ISOFORM 1/4)
                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 186-1192 FROM N.A. (ISOFORM 1)
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  (ISOFORM 3).
                      rissum=umbilical cord blood;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 409:341-346(2001)
                                                                                                                                                                                                                                                                                                                                                            TISSUE=Testis;
Sha J.H., Zhou Z.M.,
Submitted (JAN-2001)
  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein
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Usage by and for commercial
                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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veen the Swiss Institute of Bioinformatics and the EMBL outstati
European Bioinformatics Institute. There are no restrictions on
by non-profit institutions as long as its content is in no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP
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0; Mismatches
                                                                    modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1756.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BAA74909.2; ALT_INIT.
AAH01035.1; -.
                                                                                                                                                             AJ251383; CAB99248.1; -. AJ251384; CAB99249.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.0%;
30.3%;
                                                                                                                                                                                                                 CAB99250.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAG17976.1;
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                                                                                                                                                                                                                                    BAB18927.1
BAB18928.1
                                                                                                                                                                                                                                                                                     AAG12176.1
                                                                                                                                                                                                                                                                                                              AAG12177.1
                                                                                                                                                                                                                                                                                                                                  AAG12205.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAD27783.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 95.0
Best Local Similarity 30.3
Matches 361, Conservative
                                                                                                                                                                                                                                                                                                                                                        AAG40878
                                                                                                                                                                                                                                                                                                                                                                                                                               BAA83712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AB020693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BC007109;
                                                                                                                                                                                                                                                                                                              AF148538;
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                                                                                                                                                                                                                                    AB040462;
AB040463;
                                                                                                                                                                                                                                                                                                                                                          AF320999
                                                                                                                                                                                                                                                                                   AF148537
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260 YSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFS 319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EDEEEEEEEEEEEEDEDEDLEELEVLERKPAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPR
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                              12;
                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 343;
                                                                                                                                                                                                                                                                                                                                                                         90.3%; Score 1669.8; DB 2; Length
96.2%; Pred. No. 2.2e-46;
ive 0; Mismatches 1; Indels
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Van der Putten H.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
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Van der Putten H., Mir A.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                             Strausberg R.;
Submitted (UUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC071848; AAH71848.1; -.
GO; GO:0005783; C:endoplasmic reticulum; IEA.
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                                                                                                                                                                                                                        InterPro; IPR003388; Reticulon.
Pfam, PP02453; Reticulon, 1.
PROSITE; PS50465; RETICULON; 1.
SEQUENCE 343 AA; 36918 MW; 813207C29ABI5BA4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           302 VPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE
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Last annotation update)
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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J. Mol. Biol. 325:299-323(2003).
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(TrEMBLrel. 23, I
(TrEMBLrel. 27, I
                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 96.2
Matches 329; Conservative
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                                                     SEQUENCE FROM N.A.
TISSUE=Eye;
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MEDINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MAL Strausberg R. L., Feingold E. A., Grouse L. H., Derge J. G.,
MAL Schuler G.D.,
MAL S. R., Zeeberg B., Buetow K. H., Schaefer C. F., Bhat N. K.,
MOSTER, Jordan H., Moore T., Max S. I., Wang J., Hisheh F.,
MAL Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
MAL Diatchenko L., Wodin T. B., Toshiyuki S., Carninoi P., Prange C.,
MAL S. S., Loquellano N.A., Peters G. A., Abramson R. D., Mullahy S. J.,
Mosak S.A., McEwan P. J., McKernan K. J., Malek J. A., Gunaratne P. H.,
Mosak S. Morley K. C., Hale S., Garcia A. M., Gay L. J., Hulyk S. W.,
Milalon D. K., Muzny D. M., Sodergren E. J., Lu X., Gibbs R. A.,
Myllalon D. K., Muzny D. M., Sodergren E. J., Lu X., Gibbs R. A.,
Myllalon D. K., Muzny D. M., Sodergren E. J., Lu X., Gibbs R. A.,
Myllalon D. K., Muzny D. M., Sodergren E. J., Lu X., Gibbs R. A.,
Myllalon B., Rotchman J. W., Garcia A. M., Rodrigues S., Sanchez A.,
Myllalon D. K., Muzna D. W., Green E. D., Dickson M. C.,
Myers R. M., Touchman J. W., Green E. D., Dickson M. C.,
Modriguez A. C., Grimwood J., Schmutz J., Myers R. M., Butterfield Y. S.,
Modriguez A. C., Grimwood J., Schmutz J., Myers R. M.,
Modriguez A. C., Grimwood J., Schmutz J., Myers R. M.,
Modriguez A. C., Maria M. M.;
Mones S. J., Marra M. M.;

and mouse cDNA sequences.",
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                                                        661 EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE 720
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                                                                                                                                                                        721 MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMLVKESLTETSFESMI
                                                                                                                                                                                                                                                                                      791 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                     1 MEDIDQSSLVSSSADSPPRPPPAFKYQFVTEPEDEEDEEDEEDEEDEEDEEUERKEP
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                       30;
                                                                                                                                                                                                                                                            Length 375;
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Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
                                                                                                                                                                                                                                                        82.9%; Score 1533; DB 2; 82.8%; Pred. No. 7.4e-42;
                                                         GO, GO:0005783; C:endoplasmic reticulum; IDA. GO; GO:0005515; F:protein binding; IPI. GO; GO:0001525; P:angiogenesis; IMP. GO; GO:0007399; P:neurogenesis; IDA. Fiterbro; IPRO03388; Reticulon. Pfam; PF02453; Reticulon; 1.
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J. Mol. Biol. 325:299-323(2003)
EMBL; AY102282; AAM73504.1; -. EMBL; AY102286; AAM73509.1; -. MGD; MGT:1915835; Rtn4.
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(TrEMBLrel. 23, L
(TrEMBLrel. 27, L
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Matches 317; Conservative
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61 AAGLSAAPVP--PAA-APLLDFSSDSVPPAPRGPLPAAPPTAPERQPSWERSPAAS---A 114
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                 29;
                                                                                                                                                                                                                                                                                                                                                                                          Length 356;
Van der Putten H., Mir A.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AX102281; AAM73503 1; -.
EMBL; AX102286; AAM73508.1; -.
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Jin W., Li R., Long M., Shen J., Ju G.;
Jin W., Li R., Long M., Shen J., Ju G.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AY114153; AM77069.1;
GO; MGI:1915835; Rt.4.
GO; GO:0005783; C:endoplasmic reticulum; IEA.
InterPro; IPR003388; Reticulon.
                                                                                                                                                                                                                                                                                                                                356 AA; 38403 MW; 4366C03BA9630B56 CRC64;
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Last annotation update)
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84.5%; Pred. No. 1.4e-41;
iive 11; Mismatches 18
                                                                                                  MODE, MOI:1918935, Rtn4.
GO; GO:0005783; C:endoplasmic reticulum; IDA.
GO; GO:0005515, F:protein binding; IPI.
GO; GO:0001525; P:angiogenesis; IMP.
GO; GO:0007399; P:neurogenesis; IDA.
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Pfam; PF02453; Reticulon; 1.
PROSITE; PS50845; RETICULON; 1.
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PROSITE; PS50845; RETICULON, 1.
SEQUENCE 357 AA, 38566 MW.
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(TrEMBLrel. 22, L
(TrEMBLrel. 26, L
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Best Local Similarity 84.5°
Matches 315; Conservative
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227
                                                                                                                                                                                                                                                                                                                         GVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDS 287
                                                                                                                                                                                                                                                                                                                                                          283
                                                                                                                                       AAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPA 119
                                                                                                                                                                                                  PSPLSAAAVSPSKLPEDDEPPARPPPPPBASVSPQAEPVWTPPAPAPAPPSTS----- 173
                                                                                                                                                                                                                                                                                 164 GSGSVVVDLLYWRDIKKTGVVYFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYK 223
                                                                                                                                                                                                                                                                                                                                                                                        LKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMA 347
                                                                                                                                                                                                                                                                                                                                                                                                         59
                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 3), AND PARTIAL SEQUENCE.
STRAIN=Sprague-Dawley, TISSUE=Adipocyte;
MEDLINE=99249816; PubMed=10231557; DOI=10.1016/S0167-4889(99)00033-6;
MOTISE N.J., Roses S.A., Neveu J.M., Lane W.S., Lienhard G.E.;
"Cloning and characterization of a 22 kDa protein from rat adipocytes: a new member of the reticulon family.";
Biochim. Biophys. Acta 1450:68-76(1999).
                                                                                          GVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDS
                                                                                                                                                                                                                                                            ----VVDLLYWRDIKKTGVV-FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYK
                                                                        1 MEDLDQSPLVSSS-DSPPRPQPAFKYQFVREPEDEEEEEEEEEEEDEDEDLEELEVLERKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TW0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIN4 RAT STANDARD; PRT; 1163 AA.
Q9JKI1; Q9JKI0; Q9R0D9; Q9WUE9; Q9WUF0;
28-FEB-2003 (Rel. 41, Last sequence update)
28-GFB-2003 (Rel. 41, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)
(Glut4 vesicle 20 kDa protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS 2 AND 4).
STRAIN=Wistar Kyoto; TISSUE=Vascular smooth muscle;
Ito T., Schwartz S.M.;
"Cloning of a member of the reticulon gene family in rat: one of minor splice variants.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
MEDLINE=20129286; PubMed=10667796; DOI=10.1038/35000219;
Chen M.S., Huber A.B., Van der Haar M.E., Frank M., Schnell L.,
Spillmann A.A., Christ F., Schwab M.E.;
"Nogo-A is a myelin-associated neurite outgrowth inhibitor and a
                                          18; Indels 30;
            Length 357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 minor splice variants.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
           81.8%; Score 1513; DB 2;
84.2%; Pred. No. 2.9e-41;
iive 11; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for monoclonal antibody IN-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                    KIQAKIPGLKRKAE 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 344 KIQAKIPGLKRKAE 357
                         Best Local Similarity 84.2
Matches 315; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=Rtn4; Synonyms=Nogo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antigen for monoclonal a
Nature 403:434-439(2000)
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              Query Match
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                         GrandPre T., Li S., Strittmatter S.M.;
"Nogo-66 receptor attegonist peptide promotes axonal regeneration.";
Nature 417:547-551 (2002).
-!- FUNCTION: Potent neurite outgrowth inhibitor which may also help
block the regeneration of the nervous central system in adults (By
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EMBL; AF132046; AAD31019.1; -.

GO; GO:0030176; C:integral to endoplasmic reticulum membrane; IDA.

GO; GO:0005515; C:integral to endoplasmic reticulum membrane; IDA.

GO; GO:0005515; C:integral to membrane; ISS.

GO; GO:0005515; F:protein binding; ISS.

GO; GO:0019897; P:negative regulation of anti-apoptosis; ISS.

GO; GO:0030517; P:negative regulation of axon extension; ISS.

InterPro; IPR003889; Reticulon.

PROSTIE; PSS0845; RETICULON; 1.

Alternative splicing; Direct protein sequencing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity).
SUBCELLULAR LOCATION: Integral membrane protein. Anchored to
membrane of the endoplasmic reticulum through 2 putative
                                                                                                                                                                                                                                                                                                                                                                                                                 similarity).
SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2
MEDLINE=22033691; PubMed=12037567; DOI=10.1038/417547a;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=3; Synonyms=Nogo-C, VP20;
IsoId=Q9JK11-3; Sequence=VSP_005656, VSP_005657;
Name=4; Synonyms=Foocen-M2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /Fridavsp 005657.
Missing (In isoform 2).
Fridavsp 005658.
Missing (In isoform 4).
/Fridavsp_005659.
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Cytoplasmic (Potential)
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Lumenal (Potential).
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EMBL, AJ242961; CAB71027.1; --
EMBL, AJ242962; CAB71028.1; --
EMBL, AJ242963; CAB71029.1; --
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                                                                                                                                                                                           ELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDH 333
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MEDLINE=223/S40; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
MCDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
MCDLINE T., Huber C., van der Putten H., Schwab M.E.;
"Genomic structure and functional characterisation of the promoters of
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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A Van der Putten H., Mir A.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
B. Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
B. REMBL; AX102286; AMM73510.1; -.
DR RGD; AX102286; AMM73511.1; -.
DR GO; GO:0005783; Rtn4.
GO; GO:0005515; Fiprotein binding; IPI.
DR GO; GO:0001525; P:nordiogenesis; IMP.
DR GO; GO:0001525; P:nordiogenesis; IMP.
DR GO; GO:0001525; P:nordiogenesis; IMP.
DR GO; GO:0007399; P:neurogenesis; IMP.
DR GO; GO:0004545; Reticulon.
DR Pfam; PF00453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
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Last annotation update)
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J. Mol. Biol. 325:299-323(2003)
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(TrEMBLrel. 23, I
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Van der Putten H.;
Submitted (MAY-2002)
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Matches 319; Conserv
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                                                                                                                                                             Gaps
                                                                                          ; Score 1478.8; DB 1; Length 1163; ; Pred. No. 6.1e-39; 11; Mismatches 25; Indels 812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APSPLSAAAVSPSKLPEDDEPPARPPPPPASVSPQAEPVWTPPAPA-----
1130 1131 Missing (in Ref. 3; AAD31020).
1163 AA; 126386 MW; 8CB894B09E94F0B6 CRC64;
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                                                                                          79.9%;
27.4%;
                                                                                                                        Best Local Similarity 27.49
Matches 320, Conservative
CONFLICT
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AC 08K3G8; DT 01-OCT-2002 (TrEMBLrel. 22, Created) DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update) DT 01-OCT-2002 (TrEMBLrel. 26, Last annotation update) DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) DE Nago-A. GN Name=Rtn4; GN Name=Rtn4; OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Wammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. OC NCBI_TAXID=10090; RN 11] RP SEQUENCE FROM N.A. STRAIN=BALB/c; RA 31n W., Long M., Li R., Ju G.; RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases. DR MGD; MII:1915835; RAM77068.1; DR MGD; MII:1915835; RAM77068.1; DR MGD; MII:1915835; RAM77068.1; DR MGD; MII:1915835; RAM77068.1; DR MGD; MII:1915835; RAM77068.1; DR MGD; MII:1915835; RAM77068.1; DR MGD; MII:1915835; RAM77068.1; DR MGD; MII:1915835; RAM77068.1; DR MGD; MGCF08.2. CANADARA	GG) GG:00007843; Cendoophasmic reticulum; InterPro; IPR003388; Reticulon. Pfam; PF02453; Reticulon; 1. PROSITE; PS50845; RETICULON; 1. SEQUENCE 1163 AA; 126690 MW; 6B5F36279 Duery Match 77.9%; Score 1441.2; 3est Local Similarity 27.2%; Pred. No. 1e- datches 318; Conservative 11; Mismatches	1 MEDLDQSPLVSSS-DSPPRPQPAFKXQFVREPEDEEEEEEEEEBEDBEDLEELEVLER	DETL	1/3 FALPAASEPVIPSSAEKIMDLKEQPGNIVSSGQEDFPSVLFETAASLFSLSTVSFKE 169	Db 353 NEMKONSVVAPVREEYADFKPFEQAWEVKDTYEGSRDVLAARANMESKVDKKCFEDSLEQK 412 Qy 169	Qy 169 Db 533 VQEACESELNEATGTKIAYETKVDLVQTSEAIQESIYPTAQLCPSFEEAEATPSPVLPDI 592 Qy 169
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EMBL, AY123245; AAM64249.1; -.
GO; GO:0005783; C:endoplasmic reticulum; IEA.
InterPro; IPR003388; Reticulon.
Pfam; PF02453; Reticulon; 1.
PROSITE; PSS0845; RETICULON; 1.
SEQUENCE 986 AA; 108449 MW; OCDE8F6470364
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Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
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(TrEMBLrel. 27, I
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                                                                                   713 VDDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVSETVTQHKHKERLSASPQEV
                                                                                                                                                                    773 GKPYLESFQPNLHITKDAASNEIPTLTKKETISLQMEEFNTAIYSNDDLLSSKEDKMKES
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  EEIKEPESFNAAAQEAEAPYISIACDLIKETKLSTEPSPGFSNYSEIAKFEKSVPDHCEL
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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TISSUB=Testis;
Oertle T., Schwab M.E.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
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Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
8NT4 (RTM4 isoform Ab) (RTM4 isoform D) (RTM4 isoform S)
F) (RTM4 isoform G) (RTM4 isoform Aa).
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J. Mol. Biol. 325:299-323(2003).
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EMBL; AX123246; AAM64250.1; --
EMBL; AX123247; AAM64251.1; --
EMBL; AX123248; AAM64252.1; --
EMBL; AX12329; AAM64253.1; --
EMBL; AX123250; AAM64254.1; --
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TISSUE=Testis;
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667 TLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKI 726
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                                                                                                                                                                                                               DLVQTSEVMQESLYPAAQLCPSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSS 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     727 SFSDDFSKNGSATSKVLLLPPDVSALATQAEIESIVKPKVLVKEAEKKLPSDTEKEDR-- 784
                                                                                                                                                                                                                                                                                                                                                                               ----VLERKPAAGLSAAPVP-----T----TAPAAGAPLMDFGNDF 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         547 IPDVPQKQDETVMLVKESLTETSFESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKD
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                                                                                                                                                                                                                                                                                                   607 TLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFISKEAQIRETETFSDSSPIEIIDEFP
                                                                                                                                                                                                                                                                 492 ACDLIKETK----LSAEPAPDFSDYSEMAKVEQPVPDHSBLVEDSSPDS-EPVDLFSDDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145 PPPPASVSPQAEPVWTPPAPAPAPPSTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=129/SvcJ7, and 129SvcJ7;
MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
                                                                                                       Gape
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Sciurognathi; Muridae; Murinae; Mus
                                                                                                       60; Indels 300;
                                               Length 986;
986 AA; 108449 MW; 0CDE8F647036415A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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                                                  DB 2;
                                               55.6%; Score 1028; DB 2; 39.2%; Pred. No. 1.8e-24; iive 27; Mismatches 60
                                                                                                                                                            DLDQS------PLVSSSDSPPRP----
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559
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 , Huber C., van der Putten H., Schwab M.E.; structure and functional characterisation of the promoters of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         500 PLEVPSPVSYDGIKLEPENPPPYEEAMSVALKTSDSKEEIKEPESFNAAAQEAEAPYISI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 560 ACDLIKETK----LSTEPSPEFSNYSEIAKFEKSVPDHCELVDDSSPES-EPVDLFSDDS
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                                                                                                                                                                                                                                                                                                                                                                                                    Indels 278; Gaps
                                                                                                                                                                                                                                                                                                                                                                           Length 1046;
                                                                                                                                                     STRAIN-1298vc7;

1 Van der Putten H., Mir A.;

Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AX102286, AAM73502.1;

EMBL, AX102286, AAM73507.1;

MGD, MGI:1915835, Rth4.

GO; GO:00057815, F:protein binding; IPI.

GO; GO:0001525, F:angiogenesis; IMP.

GO; GO:0001525, F:angiogenesis; IMP.

GO; GO:0001525, F:neurogenesis; IMP.

GO; GO:0001525, F:neurogenesis; IMP.
                                                                                                                                                                                                                                                                                                                 Pfam; PF02453; Reticulon; 1.
PROSITE; PS50845; RETICULON; 1.
SEQUENCE 1046 AA; 114221 MW; RCE2E2238ED51222 CRC64;
                                                                                                 Van der Putten H.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             148 PASVSPQAEPVWTPPAPAPAAPPS--------
                                                                                                                                                                                                                                                                                                                                                                        53.7%; Score 994; DB 2; L. 38.6%; Pred. No. 2.6e-23; ive 31; Mismatches 73;
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                             human and mouse nogo/rtn4.";
J. Mol. Biol. 325:299-323(2003)
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Oertle T., Huber C.,
                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                           SEQUENCE FROM N.A.
                                                                       FROM N.A.
                                                                                     STRAIN=129/SvcJ7
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                                                                     SEQUENCE
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STRAIN-EVBN/N, TISSUE-Mammary tumor. C3;

MEDINB=2238825; PubMed=1247732; DOI=10.1073/pnas.242603899;

STRAIN-EVBN/N, TISSUE-Mammary tumor. C3;

RIJUINB=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;

STRAIN-EXBN.COlling F.S., Wargner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

Hopking R.F., Jordan H., Moore T., Max S.I., Wang J., Heigh F.,

Bitchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

Stapleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Willalon D.K., Muzny D.W., Sodergren B.J., Lu X., Gibbs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Schwerten D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

R. Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 278;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=FYB/N; TISSUE=Mammary tumor. C3;
Strausberg R.; SIGN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                      Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO:0005783; C:endoplasmic reticulum; IEA
                                      639 AA
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                                      PRT;
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                                                                    01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; BC032192; AAH32192.1;
MGD; MGI:1915835; Rtn4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 38.6
Matches 240; Conservative
                                      PRELIMINARY;
                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                Rtn4 protein.
                                                                                                                                                 Name=Rtn4;
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127 AVSP	TRELIMINARY; PRT; 658 AA. QGRSSB QGRSSB QGRSSB; QGRSSB; QGRSSB; QGRSSB; O5-JUL-2004 (TrEMBLrel. 27, Last sequence update) O5-JUL-2004 (TrEMBLrel. 27, Last sequence update) O5-JUL-2004 (TrEMBLrel. 27, Last sequence update) Neurite outgrowth inhibitor NOGO-A (Fragment). Name-NOGO; Gallus gallus (Chicken). Rackaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelatharyota; Metazoa; Chordata; Craniata; Vertebrata; Butelarius Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Gallus. [1] SEQUENCE FROM N.A. Calthary S.A., Pira C.U., McNeill D.S., Liwnicz B.H., Obesubmitted (DGC.) Calthary S.A., Pira C.U., McNeill D.S., Liwnicz B.H., Obesubmitted (DGC.) COCONOS783; C:endoplasmic reticulum; IEA. InterPro; IPROMS18; Reticulon; Pfan; PFOOA53; Reticulon; 1. PROSITE; PSSO845; RETICULON; 1. NON TER 1 11 SEQUENCE 658 AA; 72075 MW; 1487A000CSEBCDAS CRC64;	Query Match

268 ASNEIPTLTKKETISLOMEEFNTAI 123 ISAAAVSP	KSVKDAMAKIQAKIPGLKRKAE PRELIMINARY; E 003 (TrEMBLrel. 24, Las 003 (TrEMBLrel. 25, Las Eragment). 14 (Mouse). 2 Metazoa; Chordata; C 2 intheria; Rodentia; C 1D=10090; FROM N.A. 4 Hirata T.; 6 (OCT-2001) to the EME 7 (OCT-201) to the EME 105783; C:endoplasmic x 1 IPR003388; Reticulon. 1 PSS0845; RETICULON; 1.	Query Match

Job time : 119.158 secs

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242
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310 AMEPKPGDSKGLSPS-----SPVSVEDDFVMLVDPKTGTEFVAEVTDRETVHKNESKD 362
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                                                                363 ISNEIRDEKRQAPLTELPCDLSVRNVEVKTEDDAHALKKSLQAIDREVPEVSMV---SLP
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"A reticular rhapsody: phylogenic evolution and nomenclature of the RTN/Nogo gene family.";
EASEB J. 17:1238-1247(203).
EMBL; AN164744; AAP47319.2; -.
GO; GO:0005783; C:endoplasmic reticulum; IEA.
InterPro; IPR003388; Reticulon.
Pfam; PF02453; Reticulon, 1.
PROSITE; PS50845; RETICULON; 1.
SEQUENCE 199 AA; 22395 MW; C60161DF3FB34D80 CRC64;
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.
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Pred. No. 8e-23;
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ilarity 100.0%; Pred. No. 8e-
Conservative 0; Mismatches
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MEDLINE=22715887; PubMed=12832288;
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01-OCT-2003 (TrEMBLrel. 25,
01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
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PGLKRKAE 199
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Name=RTN4;
Bos taurus (Bovine).
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Best Local Similarity
Matches 188; Conserv
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NCBI_TaxID=9913;
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